

<SPONSOR>593

<CATEGORY>IM2-06

<TITLE>Anti-idiotypic-cytokine fusion protein for breast cancer therapy.

<LAST>Tripathi

<INIT>P.K.

<LAST>Qin

<INIT>H-X.

<LAST>Xu

<INIT>C.

<LAST>Foon

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<ABSTRACT>We have generated a murine monoclonal anti-idiotypic antibody, 11D10, which mimicks biologically and antigenically a distinct and specific epitope of the high molecular weight human milk fat globule (HMFG). To augment the immunogenicity of 11D10 in vaccinated breast cancer patients, without using any carrier protein or adjuvant, we made a chimeric 11D10-GM-CSF fusion protein vaccine. An expression plasmid was made by ligation of the sequences of 11D10 light chain variable region, upstream of human κ constant region. The heavy chain plasmid was made by ligation of the heavy chain variable region sequences upstream of human γ 1 constant region CH1 and DNA fragment encoding the mature GM-CSF peptide to the 3' to the CH3 exon. P3 plasmocytoma cells were transfected with the light and heavy chain vectors by electroporation. Fusion protein was purified from culture media by chromatography in protein A columns and was separated on 7.5% non-reducing and 12.5% reducing SDS-polyacrylamide gels for western blotting. In non-reducing gel, a single band ~180 kd reacted with anti-human κ , anti-human λ 1 and anti-GM-CSF antibodies. In the reducing gel, a ~74 kd protein reacted with anti-human λ 1 and anti-GM-CSF antibodies. The fusion protein induced proliferation of GM-CSF dependent NFS-60 cells and strongly bound to anti-HMFG monoclonal antibody (Ab1). These results suggest that the protein is a chimeric anti-idiotypic antibody consisting of 11D10 variable domains, human κ and λ 1 constant domains. GM-CSF molecule is fused to γ 1 and is biologically active. Supported in part by NIH grant 1U01 CA 65748.

S. Chatterjee

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===== 2179
Return-Path: <blastmai@BLASTER.NLM.NIH.GOV>
Received: from UKCC (NJE origin SMTP@UKCC) by UKCC.UKY.EDU (LMail V1.2a/1.8a) with BSMTMP id 3791; Fri,
19 Jan 1996 17:33:18 -0500
Received: from ncbi.nlm.nih.gov by UKCC.uky.edu (IBM VM SMTP V2R3) with TCP;
Fri, 19 Jan 96 17:33:13 EST
Received: from blaster.nlm.nih.gov by ncbi.nlm.nih.gov
id RAA01409; Fri, 19 Jan 1996 17:33:11 -0500
Received: by blaster.nlm.nih.gov (950511.SGI.8.6.12.PATCH526/5.6)
id RAA09963; Fri, 19 Jan 1996 17:33:09 -0500
Date: Fri, 19 Jan 1996 17:33:09 -0500
Message-Id: <199601192233.RAA09963@blaster.nlm.nih.gov>
To: SKCHAT00@UKCC.uky.edu
Subject: Results-BLAST Server
From: NCBI BLAST E-Mail Server <blast@ncbi.nlm.nih.gov>
Errors-To: <owner-blast@ncbi.nlm.nih.gov>
Reply-To: "NCBI BLAST E-Mail Server" <blast@ncbi.nlm.nih.gov>
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==+=====
To Obtain Documentation: send an e-mail message to 'blast@ncbi.nlm.nih.gov'
with the word HELP in the body of the message. The documentation was last
modified March 18th.
```

```
==+=====
March 18, 1995
The BLAST FAQ was updated with the question Q33 related to degenerated
nucleotide code available for the BLAST programs.
```

```
==+=====
August 8, 1995
A new server directive ACKNOWLEDGE, has been added to the server. See the
help file for more details.
```

```
Trying blaster... connected
National Center for Biotechnology Information (NCBI)
```

Experimental GENINFO(R) BLAST Network Service (Blaster)

Fri Jan 19 17:31:12 EST 1996, Up 30 days, 5:22, 1 user, load: 42.14, 39.23, 35.07

PEPTIDE SEQUENCE DATABASES

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nr Non-redundant PDB+SwissProt+PIR+SPUpdate+GenPept+GPUpdate, updated daily
for efficient, complete searches of the five component databases:
pdb Brookhaven Protein Data Bank, April 1995 Release
swissprot SWISS-PROT Release 32.0, December 1995
pir PIR Release 45.0 (complete), June 30, 1995
spupdate SWISS-PROT cumulative weekly update to the major release
genpept CDS translations from GenBank(R) Release 92, December 15, 1995
gpupdate cumulative daily updates to the major release of genpept
kabatpro Kabat Sequences of Proteins of Immunological Interest, June 1995
tfd TFD transcription factor (protein) database Release 7.0, June 1993
alu * Translations of select Alu repeats from REPBASE
```

NUCLEOTIDE SEQUENCE DATABASES

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nr Non-redundant PDB+GBUpdate+GenBank+EmblUpdate+EMBL, updated daily
for efficient, complete searches of the four component databases:
pdb Brookhaven Protein Data Bank, April 1995 Release
genbank GenBank(R) Release 92 (no daily updates), December 15, 1995
gbupdate GenBank(R) cumulative daily updates to the major release
embl EMBL Data Library, Release 45.0, December 1995
emblu EMBL Data Library cumulative daily updates to the major release
vector Vector subset of GenBank(R), February 3rd, 1995
alu *+ Select Alu repeats from REPBASE
kabatnuc Kabat Sequences of Nucleic Acid of Immunological Interest, June 1995
epd Eukaryotic Promoter Database Release 43, June 1995
dbest + Database of Expressed Sequence Tags (cumulative daily update)
dbsts + Database of Sequence Tagged Sites Release 1.5, October 26, 1994
```

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You can obtain the BLAST documentation files, send a message consisting of just the word "help" (without the quotes) to: blast@ncbi.nlm.nih.gov
Last modification dates: August 10th 95 for the E-mail server help, January 19th 94 for the BLAST manual and March 18th 95 for the BLAST FAQ.

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For a free subscription to "NCBI News", the NCBI newsletter, send a request along with your name and postal mailing address to: info@ncbi.nlm.nih.gov

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A new GenBank sequence submission tool, called BankIt, is now available through the NCBI's home page on the World Wide Web. The URL is <http://www.ncbi.nlm.nih.gov>

[illegible]

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0.0040 3697 45 |=====
0.0025 3652 39 |=====
0.0016 3613 35 |=====

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Sequences producing High-scoring Segment Pairs:				High Score	Smallest Sum Probability P(N)	N
gb L48668 MUSY	Mus musculus (cell line C3H/F2-20) c...	1337	2.9e-123	2		
gb L48680 MUSAL	Mus musculus (cell line C3H/F2-3) ch...	1301	1.3e-120	2		
emb X64805 MMAIDHCH	M.musculus mRNA for anti-Id mAB 114 ...	1473	2.6e-117	1		
gb M17953 MUSIGHXW	Mouse Ig rearranged H-chain V-region...	1350	1.7e-114	2		
gb I05921 I05921	Sequence 37 from patent EP 0274394. ...	1350	4.4e-114	2		
emb Z22117 MDIGGVBC	M.domesticus IgG variable region.	1127	7.4e-106	2		
gb M15224 MUSIGLAF	Mouse IgM H-chain lambda rearranged ...	1106	4.1e-104	2		
gb M15226 MUSIGLAH	H-chain lambda rearranged anti-Dns h...	1101	1.0e-103	2		
gb M15225 MUSIGLAG	H-chain lambda rearranged anti-Dns h...	1101	1.1e-103	2		
gb M20835 MUSIGKCLP	Mouse IgMk rearranged heavy-chain mR...	1093	3.8e-103	2		
emb Z22034 MDIGGVAG	M.domesticus IgG variable region.	1075	5.9e-103	2		
emb X59180 MMIGHT457	Mouse immunoglobulin variable region...	1098	7.3e-103	2		
emb Z25449 MMIGGCVRE	M.musculus immunoglobulin gamma heav...	1299	9.1e-103	1		
emb Z25457 MMIGGCVRI	M.musculus immunoglobulin gamma heav...	1298	1.1e-102	1		
gb L08216 MUSANTDNAK	Mouse anti-DNA antibody heavy chain ...	1098	4.7e-102	2		
emb A13735 A13735	variable region of a monoclonal anti...	1046	1.2e-101	2		
gb M20274 MUSIGHKA	Mouse Ig active gamma chain mRNA V-r...	1155	1.2e-101	2		
gb M32037 MUSIGHRK	Mouse Ig H-chain mRNA V-D-J region, ...	1155	1.2e-101	2		
gb M28834 MUSIGHALPA	Mus musculus IgG2a chain (anti-Pseud...	1046	1.2e-101	2		
gb M36225 MUSIGHAEF	Mouse Ig heavy-chain mRNA V region, ...	1284	1.4e-101	1		
gb U39781 MMU39781	Mus musculus J558+ IgM heavy chain m...	1073	2.3e-101	2		
emb Z25447 MMIGGCVRD	M.musculus immunoglobulin gamma heav...	1282	2.4e-101	1		
emb X65773 MMLB4IHEV	M.musculus DNA for IgE antibody heav...	1279	2.8e-101	1		
gb U23046 MMU23046	Mus musculus, clone 2C10 anti-ds-DNA...	1071	3.2e-101	2		
emb Z12765 MM37F2A	M.musculus mRNA for VH-gen sequence ...	1086	3.9e-101	2		
gb U10410 MMU10410	Mus musculus recombinant antineurami...	1191	4.7e-101	2		
gb M32036 MUSIGHRJ	Mouse Ig H-chain mRNA V-D-J region, ...	1146	6.8e-101	2		
emb Z68170 MMVAR605	M.musculus mRNA for immunoglobulin h...	1065	1.0e-100	2		
gb L08220 MUSANTDNAO	Mouse anti-DNA antibody heavy chain ...	1071	1.5e-100	2		
gb M19292 MUSIGHXK	Mouse IgG active H-chain gene VDJ2-r...	1142	1.5e-100	2		
emb Z22028 MDIGGVAD	M.domesticus IgG variable region.	1071	1.8e-100	2		
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gb M61026 MUSIGHAANN	M.musculus Ig rearranged H-chain mRN...	1266	4.4e-100	1		
emb Z12794 MMV20552B	M.musculus mRNA for VH-gen sequence ...	1057	4.5e-100	2		
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emb Z22129 MDIGMVBC	M.domesticus IgM variable region.	1057	4.6e-100	2		
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gb M64141 MUSIGHNOL	Mouse Ig active heavy-chain mRNA V-r...	1046	8.8e-100	2		
gb I09505 I09505	Sequence 3 from patent WO 8909622.	1107	9.8e-100	2		
gb M31908 MUSIGHRC	Mouse Ig H-chain V-D-J region mRNA, ...	1132	9.9e-100	2		
gb M28251 MUSIGHMX	Mouse Ig rearranged gamma-chain (G-2...	1107	1.1e-99	2		
emb Z12783 MMV20292B	M.musculus mRNA for VH-gen sequence ...	1052	1.2e-99	2		
gb M36215 MUSIGHADV	Mouse Ig heavy-chain mRNA V region, ...	1060	1.2e-99	2		
emb A23297 A23297	M.musculus CTM01 monoclonal antibody...	1073	1.5e-99	2		

emb	Z12798	MMV20642B	M.musculus mRNA for VH-gen sequence ...	1048	2.5e-99	2
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emb	X68118	MMIGHPS4A	M.musculus gene for IG heavy chain (...)	1122	6.6e-99	2
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emb	X75100	MMASWU1H	M.musculus (A.SW) mRNA for ASWU1 ant...	1130	1.0e-98	2
emb	Z22059	MDIGGVAN	M.domesticus IgG variable region.	1114	1.2e-98	2
gb	M12809	MUSIGHJA	Mouse Ig rearranged H-chain V-region...	1119	1.2e-98	2
emb	X56936	MMSP6718	Mouse rearranged Sp6-718 gene for Ig...	1110	1.4e-98	2
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gb	M64134	MUSIGHNOE	Mouse Ig active heavy-chain mRNA V-r...	1084	1.5e-98	2
gb	J04548	MUSIGHVBE	Mouse Ig active gamma-1-chain mRNA, ...	1114	1.7e-98	2
emb	Z25445	MMIGGCVRG	M.musculus immunoglobulin gamma heav...	1247	2.1e-98	1
gb	J04547	MUSIGHVBD	Mouse Ig active gamma-2a mRNA, VNDJ2...	1114	2.5e-98	2
emb	Z25443	MMIGGCVRB	M.musculus immunoglobulin gamma heav...	1246	2.5e-98	1
emb	Z22099	MDIGGVAV	M.domesticus IgG variable region.	1115	2.5e-98	2
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emb	X68122	MMIGHPS6A	M.musculus gene for IG heavy chain (...)	1114	3.0e-98	2
gb	M83098	MUSIGHM195	Mus musculus Ig heavy chain mRNA V-r...	1039	3.3e-98	2
gb	M64142	MUSIGHNOM	Mouse Ig active heavy-chain mRNA V-r...	1083	4.9e-98	2
gb	L08985	MUSIGVAAM	Mus musculus Ig rearranged anti-Sm h...	622	6.2e-98	4
emb	X68112	MMIGHPS1A	M.musculus gene for IG heavy chain (...)	1110	6.6e-98	2
emb	Z12763	MM2F2A	M.musculus mRNA for VH-gen sequence ...	1239	7.7e-98	1
emb	Z25451	MMIGGCVRG	M.musculus immunoglobulin gamma heav...	1240	7.7e-98	1
gb	M31956	MUSIGHRO	Mouse Ig active mu-chain mRNA V-D-J2...	1109	7.9e-98	2
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emb	Z12789	MMV20442B	M.musculus mRNA for VH-gen sequence ...	1029	9.7e-98	2
gb	L35315	MUSIVDJA	Mus musculus germline immunoglobulin...	1107	9.9e-98	2
gb	U26469	MMU26469	Mus musculus nucleosome-reactive mon...	1037	1.2e-97	2
gb	S72514	S72514	anti-estradiol antibody heavy chain ...	1024	1.3e-97	2
gb	L25855	MUSIGGB	Mus musculus IgG heavy chain gene, V...	1101	1.7e-97	2
gb	S69279	S69279	IgVH=anti-louping ill virus antibody...	1081	2.1e-97	2
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gb	L22749	MUS1	Mus musculus immunoglobulin heavy ch...	1230	4.3e-97	1
gb	U41425	MMU41425	Mus musculus monoclonal antibody FC1...	1114	5.7e-97	2
emb	Z21788	MMIGGAA	M.musculus Biozzi immunoglobulin gam...	1019	6.2e-97	2
gb	S74051	S74051	Ig VH=anti-cardiolipin immunoglobuli...	1228	6.5e-97	1
gb	U22903	MMU22903	Mus musculus anti-human interferon-g...	1076	7.4e-97	2
emb	X68120	MMIGHPS5A	M.musculus gene for IG heavy chain (...)	1096	9.4e-97	2
gb	L48669	MUSZ	Mus musculus (cell line C3H/F2-21) c...	1025	1.2e-96	2
gb	J04546	MUSIGHVBC	Mouse Ig active gamma-2a-chain mRNA,...	1094	1.4e-96	2
gb	U26470	MMU26470	Mus musculus nucleosome-reactive mon...	1017	1.4e-96	2
emb	X68114	MMIGHPS2A	M.musculus gene for IG heavy chain (...)	1092	2.0e-96	2
emb	X65004	MMIHLG43	M.musculus rearranged immunoglobulin...	1037	2.4e-96	2
emb	Z12771	MM7A1	M.musculus mRNA for VH-gen sequence ...	1221	2.4e-96	1
gb	U20819	MMU20819	Mus musculus Ig Fab F9.13.7 heavy ch...	1001	2.6e-96	2
emb	X03088	MMIGMU32	Mouse rearranged V(H) gene VMU-3.2 V...	1091	2.6e-96	2

WARNING: Descriptions of 4914 database sequences were not reported due to the limiting value of parameter V = 100.

>gb|L48668|MUSY Mus musculus (cell line C3H/F2-20) chromosome 12 anti-DNA antibody heavy chain mRNA.
Length = 357

Plus Strand HSPs:

Score = 1337 (369.4 bits), Expect = 2.9e-123, Sum P(2) = 2.9e-123
Identities = 279/294 (94%), Positives = 279/294 (94%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60

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Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGA 294
Sbjct: 241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGA 294

Score = 221 (61.1 bits), Expect = 2.9e-123, Sum P(2) = 2.9e-123
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
|||||
Sbjct: 312 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

>gb|L48680|MUSAL Mus musculus (cell line C3H/F2-3) chromosome 12 anti-DNA
antibody heavy chain mRNA.
Length = 360

Plus Strand HSPs:

Score = 1301 (359.5 bits), Expect = 1.3e-120, Sum P(2) = 1.3e-120
Identities = 277/298 (92%), Positives = 277/298 (92%), Strand = Plus / Plus

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Query:      1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCTCTGGGGCCTCAGTGAAGATG  60
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Query:     61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCAGCTGGGTAAGCAGACA  120
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Sbjct:     61 TCCTGCAAGGCTTCTGGCTACAGATTTACCAGTTACAATATGCAGCTGGGTAAGCAGACA  120

Query:    121 CCTGGACAGGGCCTGGAATGGATTGAAATATTTTCTGGAATGGTGATCTTACTAC  180
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Query:    181 AATCAGAAGTTTAAAGGCAAGGCCCTCATTGACTGCAGACACATCTCCAGCACAGCCTAC  240
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Score = 225 (62.2 bits), Expect = 1.3e-120, Sum P(2) = 1.3e-120
Identities = 53/63 (84%), Positives = 53/63 (84%), Strand = Plus / Plus

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Sbjct:   298 AGGGTAAC TACGTAGG ACATATG GACTACT GGGGTCA AGGAACCT CAGTCACC GTCTCC   357
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Query:   352 TCA   354
          |||
Sbjct:   358 TCA   360
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>emb|X64805|MMAIDHCH M.musculus mRNA for anti-Id mAB 114 heavy chain, variable region
Length = 354

Plus Strand HSPs:

Score = 1473 (407.0 bits), Expect = 2.6e-117, P = 2.6e-117
Identities = 321/354 (90%), Positives = 321/354 (90%), Strand = Plus / Plus

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Sbjct:   1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTAAGGCTGGGTCCTCAGTGAAGATG 60

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Query:   121 CCTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTAC 180
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Sbjct:   181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240

Query:   241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 300
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Sbjct:   241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAT 300

Query:   301 TGGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
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Sbjct:   301 TACTCCGTTAGTATAGACTACTGGGGCCAAGGCACCACTCTCAGTCTCCTCA 354

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>gb|M17953|MUSIGHXW Mouse Ig rearranged H-chain V-region mRNA VJ1.
Length = 458

Plus Strand HSPs:

Score = 1350 (373.0 bits), Expect = 1.7e-114, Sum P(2) = 1.7e-114
Identities = 282/297 (94%), Positives = 282/297 (94%), Strand = Plus / Plus

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Query:   121 CCTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTAC 180
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Sbjct:   276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335

Query:   241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG 297
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:   336 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGTG 392

```

Score = 101 (27.9 bits), Expect = 1.7e-114, Sum P(2) = 1.7e-114
Identities = 25/31 (80%), Positives = 25/31 (80%), Strand = Plus / Plus

```

Query:   321 CTGGGGTCAAGGAACCTCAGTCACCGTCTCC 351
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:   428 CTGGGGCACAGGGACCACGGTCACCGTCTCC 458

```

>gb|I05921|I05921 Sequence 37 from patent EP 0274394. >gb|I08811|I08811
Sequence 12 from patent WO 8804936. >gb|I09199|I09199 Sequence 38
from patent WO 8900999.
Length = 458

Plus Strand HSPs:

Score = 1350 (373.0 bits), Expect = 4.4e-114, Sum P(2) = 4.4e-114
Identities = 282/297 (94%), Positives = 282/297 (94%), Strand = Plus / Plus

```
Query:   1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
          |||||
Sbjct:  96 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 155

Query:   61 TCCTGCAAGGCTTCTGGCTACACATTGACCAAGTACAATATGCACTGGGTAAAGCAGACA 120
          |||||
Sbjct:  156 TCCTGCAAGGCTTCTGGCTACACATTGACCAAGTACAATATGCACTGGGTAAAGCAGACA 215

Query:   121 CCTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTAC 180
          |||||
Sbjct:  216 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCTTAC 275

Query:   181 AATCAGAAGTTTAAGGGCAAGGCCTATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
          |||||
Sbjct:  276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335

Query:   241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG 297
          |||||
Sbjct:  336 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGTG 392
```

Score = 96 (26.5 bits), Expect = 4.4e-114, Sum P(2) = 4.4e-114
Identities = 24/30 (80%), Positives = 24/30 (80%), Strand = Plus / Plus

```
Query:   321 CTGGGGTCAAGGAACCTCAGTCACCGTCTC 350
          |||||
Sbjct:  428 CTGGGGCACAGGGACACGGTCACCGTCTC 457
```

>emb|222117|MDIGGVBC M.domesticus IgG variable region.
Length = 360

Plus Strand HSPs:

Score = 1127 (311.4 bits), Expect = 7.4e-106, Sum P(2) = 7.4e-106
Identities = 258/300 (86%), Positives = 259/300 (86%), Strand = Plus / Plus

```
Query:   2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61
          |||||
Sbjct:  2 AGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAAGTGAAGATAT 61

Query:   62 CCTGCAAGGCTTCTGGCTACACATTGACCAAGTACAATATGCACTGGGTAAAGCAGACAC 121
          |||||
Sbjct:  62 CCTGCAAGGCTTCTGGATACACATTCACTGACTACTACATGCACTGGGTAAAGCAGAAGC 121

Query:   122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
          |||||
Sbjct:  122 CTGGGCAGGGCCTTGAGTGGATTGGAGAGATTATCCTGGAAGTGGTAATACTTACTACA 181

Query:   182 ATCAGAAGTTTAAGGGCAAGGCCTATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
          |||||
Sbjct:  182 ATGAGAAGTTCAAGGGYAAGGCCTCACTGACTGCAGACAAATCCTCCAGCACAGCCTACA 241

Query:   242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAGT 301
          |||||
Sbjct:  242 TGCAGCTCAGCAGCCTGACATCTGAGGACTCTGAGTCTATTTCTGTGCAAGACGTTACT 301
```


Score = 221 (61.1 bits), Expect = 7.4e-106, Sum P(2) = 7.4e-106
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
|||||
Sbjct: 315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

>gb|M15224|MUSIGLAF Mouse IgM H-chain lambda rearranged anti-Dns hybridoma VDJ4
region of J558 family mRNA.
Length = 360

Plus Strand HSPs:

Score = 1106 (305.6 bits), Expect = 4.1e-104, Sum P(2) = 4.1e-104
Identities = 254/295 (86%), Positives = 254/295 (86%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
|||||
Sbjct: 1 CAGGTTCAAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAAGTGAAGTTG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
|||||
Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAACAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
|||||
Sbjct: 121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTATCCTGGAGATGGTGATACTAGGTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
|||||
Sbjct: 181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCCTCCAGCACAGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAG 295
|||||
Sbjct: 241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAG 295

Score = 221 (61.1 bits), Expect = 4.1e-104, Sum P(2) = 4.1e-104
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
|||||
Sbjct: 315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

>gb|M15226|MUSIGLAH H-chain lambda rearranged anti-Dns hybridoma VDJ4 region of
J558 family mRNA.
Length = 363

Plus Strand HSPs:

Score = 1101 (304.2 bits), Expect = 1.0e-103, Sum P(2) = 1.0e-103
Identities = 253/294 (86%), Positives = 253/294 (86%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
|||||
Sbjct: 1 CAGGTTCAAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAAGTGAAGTTG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
|||||
Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAACAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
|||||
Sbjct: 121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTATCCTGGAGATGGTGATACTAGGTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
|||||

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294

Sbjct: 241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294

Score = 221 (61.1 bits), Expect = 1.0e-103, Sum P(2) = 1.0e-103
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

Subjct: 318 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCA 363

>gb|M15225|MUSIGLAG H-chain lambda rearranged anti-Dns hybridoma VDJ4 region of J558 family mRNA.
Length = 357

Plus Strand HSPs:

Score = 1101 (304.2 bits), Expect = 1.1e-103, Sum P(2) = 1.1e-103
Identities = 253/294 (86%), Positives = 253/294 (86%), Strand = Plus / Plus

Sbjct: 1 CAGGTT CAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60

[illegible]

Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAAACAGAGG 120

[illegible]

Sbjct: 121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAGATGGTGATACTAGGTAC 180

[illegible]

Sbjct: 181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCCTCCAGCACAGCCTAC 240

247 KTGACATGAGGAGGGTGAATGTGAGAGTTGTGGGCTATTTCCTGCGAGA 294
||||| ||||| | ||||| ||||| |||||

Sbjct: 241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294

Score = 221 (61.1 bits), Expect = 1.1e-103, Sum P(2) = 1.1e-103
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

[illegible]

Sbjct: 312 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

>gb|M20835|MUSIGKCLP Mouse IgMk rearranged heavy-chain mRNA variable region
(V-D-J) anti-DNA autoantibody.
Length = 462

Plus Strand HSPs:

Score = 1093 (302.0 bits), Expect = 3.8e-103, Sum P(2) = 3.8e-103
Identities = 253/296 (85%), Positives = 253/296 (85%), Strand = Plus / Plus

[illegible]

Sbjct: 106 CAGGTCCAAGTGCAGCAGCCTGGTGCTGAGCTTGTGAAGCCTGGGGCCTCAGTGAAGCTG 165

|||||

Sbjct: 166 TCCTGCAAGGCTTCTGGCTACACTTTCACCAGCTACTGGATAAACTGGGTGAAGCAGAGG 225

```

Query:   121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:   226 CCTGGACAAAGGCCCTGAGTGGATTGGAATATTTATCTGGTAGTAGTAGTACTAACTAC 285

Query:   181 AATCAGAAGTTTAAAGGCAAGGCCCTATTGACTGCAGACACATCTCCAGCACAGCCTAC 240
          |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:   286 AATGAGAAGTTCAAGAGCAAGGCCCACTGACTGTAGACACATCTCCAGCACAGCCTAC 345

Query:   241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGG 296
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:   346 ATGCAGCTCAGCAGCCTGACATCTGACGACTCTGCGGTCTATTATTGTGCAAGACG 401

Score = 221 (61.1 bits), Expect = 3.8e-103, Sum P(2) = 3.8e-103
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

Query:   309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:   417 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 462

```

```
>emb|Z22034|MDIGGVAG M.domesticus IgG variable region.  
Length = 357
```

Plus Strand HSPs:

```

Score = 1075 (297.0 bits), Expect = 5.9e-103, Sum P(2) = 5.9e-103
Identities = 251/296 (84%), Positives = 251/296 (84%), Strand = Plus / Plus

Query:      1  CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
              |||||
Sbjct:      1  CAGGTCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGAGCTTCAGTGAAGCTG 60

Query:      61  TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
              |||||
Sbjct:      61  TCCTGCAAGGCTTCTGGCTACACCTTCACTGACTATACTATACACTGGGTGAAGCAGAGT 120

Query:      121 CCTGGACAGGGCCTGGAATGGATTGAAATATTTTCTCGAAATGGTGATACTTACTAC 180
              |||||
Sbjct:      121 CCTGGACAGGGACTTGAGTGGATTGGATGGATTATCCTGGAAGTGGTAATACTAAGTAC 180

Query:      181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
              |||||
Sbjct:      181 AATGACAAGTTCAAGGGCAAGGCCACAATGACTGCAGACAAATCCTCCAGCACAGCCTAC 240

Query:      241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGG 296
              |||||
Sbjct:      241 ATGCAGCTCAGCAGCCTGACCTCTGAGGATTCTGCGGTCTATTCTGTGCAAGAGG 296

```

Score = 238 (65.8 bits), Expect = 5.9e-103, Sum P(2) = 5.9e-103
Identities = 50/53 (94%), Positives = 50/53 (94%), Strand = Plus / Plus

Query: 302 GGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
|||||
Sbjct: 305 GGGGGAGTGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

```
>emb|X59180|MMIGHT457 Mouse immunoglobulin variable region heavy chain (T4-57)
      mRNA
      Length = 350
```

Plus Strand HSPs:

Score = 1098 (303.4 bits), Expect = 7.3e-103, Sum P(2) = 7.3e-103
Identities = 254/297 (85%), Positives = 254/297 (85%), Strand = Plus / Plus

Query: 13 CAGCAGTCTGGGGCTGAGCTGGTGAGGCTCTGGGGCCTCAGTGAAGATGTCTCTGCAAGGCT 72
|||||
Sbjct: 3 CAGCAGTCTGGGCTCAGCTGGTGAGGCTGGAGCTTCAGTGAAGCTGTCTCTGCAAGGCT 62

Query: 73 TCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGACAGGGC 132
 |||||
 Sbjct: 63 TCTGGCTACACATTCAACAGCTACTGGATGCACTGGGTGAAGCAGAGGCATGGACAAGGC 122

Query: 133 CTGGAATGGATTGGAAATATTTTCTCTGGAATGGTGATACTTACTACAATCAGAAGTTT 192
 |||||
 Sbjct: 123 CTTGAGTGGATTGGAAATATTTATCCTGGTAGTGGTAGTACTAAGTACGATGAGAAGTTC 182

Query: 193 AAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGATCAGC 252
 |||||
 Sbjct: 183 AAGAGCAAGGGCACACTGACTGTAGACACATCCTCCAGCACAGCCTACATGCACCTCAGC 242

Query: 253 AGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAGTGGGAGGGT 309
 |||||
 Sbjct: 243 AGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTACAAGAGAGGAGGATGATGGT 299

Score = 214 (59.1 bits), Expect = 7.3e-103, Sum P(2) = 7.3e-103
 Identities = 46/50 (92%), Positives = 46/50 (92%), Strand = Plus / Plus

Query: 305 AGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 301 ACGGGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCAGTCTCTCCTCA 350

>emb|225449|MMIGGCVRE M.musculus immunoglobulin gamma heavy chain (DBA/1) gene,
 v region.
 Length = 305

Plus Strand HSPs:

Score = 1299 (358.9 bits), Expect = 9.1e-103, P = 9.1e-103
 Identities = 275/294 (93%), Positives = 275/294 (93%), Strand = Plus / Plus

Query: 8 ATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCCTGCA 67
 |||||
 Sbjct: 8 AACTGCAGCAGCCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCA 67

Query: 68 AGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGAC 127
 |||||
 Sbjct: 68 AGGCTTCTGGCTACACATTACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGAC 127

Query: 128 AGGGCCTGGAATGGATTGGAAATATTTTCTCTGGAATGGTGATACTTACTACAATCAGA 187
 |||||
 Sbjct: 128 AGGGCCTGGAATGGATTGAGCTATTTATCCAGGAAATGGTGATACTTCTACAATCAGA 187

Query: 188 AGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGA 247
 |||||
 Sbjct: 188 AGTTCAAGGGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGC 247

Query: 248 TCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAGT 301
 |||||
 Sbjct: 248 TCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGTTACT 301

>emb|225457|MMIGGCVRI M.musculus immunoglobulin gamma heavy chain (DBA/1) gene,
 v region.
 Length = 302

Plus Strand HSPs:

Score = 1298 (358.7 bits), Expect = 1.1e-102, P = 1.1e-102
 Identities = 274/292 (93%), Positives = 274/292 (93%), Strand = Plus / Plus

Query: 8 ATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCCTGCA 67
 |||||
 Sbjct: 8 AACTGCAGCAGCCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCA 67

```

Query:      68 AGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAGCAGACACCTGGAC 127
             |||
Sbjct:      68 AGGCTTCTGGCTACACATTACCAGTTACAATATGCACTGGGTAAGCAGACACCTGGAC 127

Query:     128 AGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTACAATCAGA 187
             |||
Sbjct:     128 AGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCTACAATCAGA 187

Query:     188 AGTTTAAGGGCAAGGCCTATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGA 247
             |||
Sbjct:     188 AGTTCAAGGGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGC 247

Query:     248 TCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAA 299
             |||
Sbjct:     248 TCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGGGA 299

```

>gb|L08216|MUSANTDNAK Mouse anti-DNA antibody heavy chain variable region (J558
VH family) mRNA.
Length = 366

Plus Strand HSPs:

Score = 1098 (303.4 bits), Expect = 4.7e-102, Sum P(2) = 4.7e-102
Identities = 254/297 (85%), Positives = 254/297 (85%), Strand = Plus / Plus

```

Query:      1  CAGGCTATCTACAGCAGCTCTGGGGCTGAGCTGGTGAGGCTCTGGGGCCTCAGTGAAGATG  60
             |||||
Sbjct:      1  CAGGTTCACTCCAGCAGCTCTGGGGCTGAGCTGGCCAGACCTGGGGCTTCAGTGAAGTTG  60

Query:     61  TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCAGCTGGGTAAAGCAGACA  120
             |||||
Sbjct:     61  TCCTGCCAGGCTTCTGGCTACACCTTTACCAGCTACTGGATGCAGTGGGTAAAACAGAGG  120

Query:    121  CCTGGACAGGGCCTGGAATGGATTGGAAATATTTTTCTGGAATGGTGATACTTACTAC  180
             |||||
Sbjct:    121  CCTGGACAGGGCCTGGAATGGATTGGGCCTATTTATCCTGGAGATGGTGATACTAGGTAC  180

Query:    181  AATCAGAAGTTTAAGGGCAAGGCCCTATTGACTGCAGACACATCTCCAGCACAGCCTAC  240
             |||||
Sbjct:    181  ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCTCCAGCACAGCCTAC  240

Query:    241  ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGG  297
             |||||
Sbjct:    241  ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTACAAGTGGG  297

```

Score = 204 (56.4 bits), Expect = 4.7e-102, Sum P(2) = 4.7e-102
Identities = 44/48 (91%), Positives = 44/48 (91%), Strand = Plus / Plus

Query: 307 GGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 319 GATGCTATGGGCTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCA 366

```
>emb|A13735|A13735 variable region of a monoclonal antibody which cross reacts
with 19 known Pseudomonas aeruginosa serotypes
Length = 540
```

Plus Strand HSPs:

Score = 1046 (289.0 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
Identities = 250/301 (83%), Positives = 250/301 (83%), Strand = Plus / Plus

```

Query:      1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCTCTGGGGCCTCAGTGAAGATG  60
             |||||  ||  |||||||||||||||||||  |||  |  |||||||||||||||||||
Sbjct:    121 CAGGTCCAGCTTCAGCAGTCTGGGGCTGAAC TGGCAAACCTGGGGCCTCAGTGAAGATG  180

Query:     61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAGCAGACA  120

```

```

Sbjct: 181 TCCTGCAAGGCTCTCGCTACACCTTTACTGCCTACTGGATGCACCTGGGTAACACAGAGG 240
Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
Sbjct: 241 CCTGGACAGGGTCTGGAATGGATTGGATACATTAATCCTAACACTGGTTATACTGAATAC 300
Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
Sbjct: 301 AATCAGAACTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC 360
Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 300
Sbjct: 361 ATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTATTGTACAAGAAGCTAC 420
Query: 301 T 301
Sbjct: 421 T 421

```

Score = 249 (68.8 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
Identities = 53/57 (92%), Positives = 53/57 (92%), Strand = Plus / Plus

Query: 298 AACTGGGAGGGTCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 424 AACTACGAGGGGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 480

>gb|M20274|MUSIGHKA Mouse Ig active gamma chain mRNA V-region VD_JH2, partial cds, clone 36-65. >gb|M20275|MUSIGHKB Mouse Ig active gamma chain mRNA V-region VD_JH2, partial cds, clone 4F8. >gb|M20276|MUSIGHKC Mouse Ig active gamma chain mRNA V-region VD_JH2, partial cds, clone 26C2. >gb|M20277|MUSIGHKD Mouse Ig active gamma chain mRNA V-region VD_JH2, partial cds, clone 24F3. >emb|X06110|MMIGVHD1 Mouse mRNA (36-35) for immunoglobulin heavy chain VD_J-region
Length = 363

Plus Strand HSPs:

Score = 1155 (319.1 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
Identities = 271/321 (84%), Positives = 271/321 (84%), Strand = Plus / Plus

```
Query:      2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      2 AGGTTCAAGCTTCAGCAGTCTGGAGCTGAGCTGGTGAGGGCTGGGTCTCAGTGAAGATGT 61

Query:     62 CCTGCAAGGCCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     62 CCTGCAAGGCCTTCTGGATATACATTCAACAAGCTACGGTATAAACTGGGTGAAACAGAGGC 121

Query:    122 CTGGACAGGGCCTGGAATGGATTGGAATATTTTTCTCGGAAATGGTGATACTTACTACA 181
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    122 CTGGACAGGGCCTGGAATGGATTGGATATATTAATCTCGGAAATGGTTATACTAAGTACA 181

Query:    182 ATCAGAAGTTTAAGGGCAAGGCCTCAT TGACTGCAGACACATCCTCCAGCACAGCCTACA 241
             || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    182 ATGAGAAGTTCAAGGGCAAGACCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACA 241

Query:    242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 301
             || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    242 TGCAGCTCAGAAGCCTGACATCTGAGGACTCTGCAGTCTATTTCTGTGCAAGATCGGTCT 301

Query:    302 GGGAGGGTGCTCTGGACTACT 322
             | | | |
Sbjct:    302 ACTATGGTGGTAGTTACTACT 322
```

Score = 142 (39.2 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
Identities = 34/41 (82%), Positives = 34/41 (82%), Strand = Plus / Plus

Query: 314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 323 TTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 363

>gb|M32037|MUSIGHRK Mouse Ig H-chain mRNA V-D-J region, from hybridoma P6514-2,
 partial cds. >gb|M32038|MUSIGHRL Mouse Ig H-chain mRNA V-D-J
 region, from hybridoma P65J4-1, partial cds.
 Length = 363

Plus Strand HSPs:

Score = 1155 (319.1 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
 Identities = 271/321 (84%), Positives = 271/321 (84%), Strand = Plus / Plus

Query: 2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61
 |||||
 Sbjct: 2 AGGTTCAAGCTTCAGCAGTCTGGAGCTGAGCTGGTGAGGGCTGGGTCTCAGTGAAGATGT 61

Query: 62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
 |||||
 Sbjct: 62 CCTGCAAGGCTTCTGGATATACATTACAAGCTACGGTATAAAGTGGGTGAAACAGAGGC 121

Query: 122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
 |||||
 Sbjct: 122 CTGGACAGGGCCTGGAATGGATTGGATATATTAATCCTGGAAATGGTTATACTAAGTACA 181

Query: 182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
 |||||
 Sbjct: 182 ATGAGAAGTTCAAGGGCAAGACCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACA 241

Query: 242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 301
 |||||
 Sbjct: 242 TGCAGCTCAGAAGCCTGACATCTGAGGACTCTGCAGTCTATTTCTGTGCAAGATCTAATT 301

Query: 302 GGGAGGGTGCTCTGGACTACT 322
 |||||
 Sbjct: 302 ACTATGGTGGTAGCTACTACT 322

Score = 142 (39.2 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
 Identities = 34/41 (82%), Positives = 34/41 (82%), Strand = Plus / Plus

Query: 314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 323 TTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 363

>gb|M28834|MUSIGHALPA Mus musculus IgG2a chain (anti-Pseudomonas aeruginosa
 lipoprotein I antibody) mRNA, 5' end.
 Length = 525

Plus Strand HSPs:

Score = 1046 (289.0 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
 Identities = 250/301 (83%), Positives = 250/301 (83%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
 |||||
 Sbjct: 106 CAGGTCAGCTTCAGCAGTCTGGGGCTGAAGTGGCAAAACCTGGGGCCTCAGTGAAGATG 165

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
 |||||
 Sbjct: 166 TCCTGCAAGGCTTCTGGCTACACCTTTACTGCCACTGGATGCACTGGGTAAACAGAGG 225

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
 |||||
 Sbjct: 226 CCTGGACAGGGTCTGGAATGGATTGGATACATTAATCCTAACACTGGTTATACTGAATAC 285

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240

Sbjct: 286 AATCAGAACTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC 345

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 300

Sbjct: 346 ATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTATTGTACAAGAAGCTAC 405

Query: 301 T 301

Sbjct: 406 T 406

Score = 249 (68.8 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
Identities = 53/57 (92%), Positives = 53/57 (92%), Strand = Plus / Plus

Query: 298 AACTGGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 409 AACTACGAGGGGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 465

>gb|M36225|MUSIGHAEF Mouse Ig heavy-chain mRNA V region, partial cds.
H280-15VH.
Length = 354

Plus Strand HSPs:

Score = 1284 (354.8 bits), Expect = 1.4e-101, P = 1.4e-101
Identities = 300/354 (84%), Positives = 300/354 (84%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60

Sbjct: 1 CAGGTCCAGCTTCAGCAGTCTGGGGCTGAACTGGCAAAACCTGGGGCCTCAGTGAAGATG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120

Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCACTGGGTAAACAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180

Sbjct: 121 CCTGGACAGGGTCTGGAATGGATTGGATACATTAATCCTAGCACTGGTTATACTGAGTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240

Sbjct: 181 AATCAGAAGTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 300

Sbjct: 241 ATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCACTGTATTACTGTGCAAGATGGGTC 300

Query: 301 TGGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 301 TATTACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

>gb|U39781|MMU39781 Mus musculus J558+ IgM heavy chain mRNA, hybridoma clone
ME2B7, partial cds.
Length = 339

Plus Strand HSPs:

Score = 1073 (296.5 bits), Expect = 2.3e-101, Sum P(2) = 2.3e-101
Identities = 245/283 (86%), Positives = 245/283 (86%), Strand = Plus / Plus

Query: 19 TCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGC 78

Sbjct: 1 TCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAAGTGAAGATGTCCTGCAAGGCTTCTGGC 60

Query: 79 TACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGACAGGGCCTGGAA 138


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Sbjct: 61 TACACCTTACCAGCTACTGGATAACCTGGGTGAAGCAGAGGCCTGGACAAGGCCTTGAG 120
Query: 139 TGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACAATCAGAAGTTAAGGGC 198
Sbjct: 121 TGGATTGGAGATATTATCCTGGTAGTGGTAGTACTAACTACAATGAGAAGTTCAAGAGC 180
Query: 199 AAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGATCAGCAGCCTG 258
Sbjct: 181 AAGGCCACACTGACTGTAGACACATCCTCCAGCACAGTCTACATGCAGCTCAGCAGCCTG 240
Query: 259 ACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 301
Sbjct: 241 ACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATGGATCT 283

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Score = 221 (61.1 bits), Expect = 2.3e-101, Sum P(2) = 2.3e-101
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

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Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
Sbjct: 294 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 339

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>emb|225447|MMIGCVRD M.musculus immunoglobulin gamma heavy chain (DBA/1) gene,
v region.
Length = 303

Plus Strand HSPs:

Score = 1282 (354.2 bits), Expect = 2.4e-101, P = 2.4e-101
Identities = 270/287 (94%), Positives = 270/287 (94%), Strand = Plus / Plus

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Query: 8 ATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCCTGCA 67
Sbjct: 8 AACTGCAGCAGCCTGGGGCTGAGCTGGTGAGCCTGGGGCCTCAGTGAAGATGTCCTGCA 67
Query: 68 AGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGAC 127
Sbjct: 68 AGGCTTCTGGCTACACATTACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGAC 127
Query: 128 AGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACAATCAGA 187
Sbjct: 128 AGGGCCTGGAATGGATTGGAGCTATTATCCAGGAAATGGTGATACTTCTTACAATCAGA 187
Query: 188 AGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGA 247
Sbjct: 188 AGTTCAAGGGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGC 247
Query: 248 TCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294
Sbjct: 248 TCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294

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>emb|X65773|MMLB4IHEV M.musculus DNA for IgE antibody heavy chain (VDJ)
Length = 451

Plus Strand HSPs:

Score = 1279 (353.4 bits), Expect = 2.8e-101, P = 2.8e-101
Identities = 299/353 (84%), Positives = 299/353 (84%), Strand = Plus / Plus

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Query: 2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61
Sbjct: 99 AGGTCCAGCTTCAGCAGTCTGGAGCTGAGCTGGTGAGGCCTGGGTCTCAGTGAAGATGT 158
Query: 62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
Sbjct: 159 CCTGCAAGAGTTCTGGATATACATTACAAGCTACGGTATAAACTGGGTGAAGCAGAGGC 218

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Query: 122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
 |||||
 Sbjct: 219 CTGGACAGGGCCTGGAATGGATTGGATATATTTATATTGGATATGGTTATATTGAGTATA 278
 |||||
 Query: 182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
 |||||
 Sbjct: 279 ATGAGAAGTTCAAGGGCAAGGCCACACTGACTTCAGACACATCCTCCAGGACAGCCTACA 338
 |||||
 Query: 242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAGT 301
 |||||
 Sbjct: 339 TGCAACTCAGCAGCCTGACATCTGAGGACTCTGCAATCTATTTCTGTGCAAGATGGGGCT 398
 |||||
 Query: 302 GGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 399 TAATCTTTGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 451
 |||||

>gb|U23046|MMU23046 Mus musculus, clone 2C10 anti-ds-DNA immunoglobulin heavy
 chain V region, partial cds.
 Length = 360

Plus Strand HSPs:

Score = 1071 (295.9 bits), Expect = 3.2e-101, Sum P(2) = 3.2e-101
 Identities = 251/297 (84%), Positives = 251/297 (84%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
 |||||
 Sbjct: 1 CAGGTCCAACCTACAGCAGCCTGGTGCTGAGCTTGGAAGCCTGGGGCCTCAGTGAAGCTG 60
 |||||
 Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
 |||||
 Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACTTTCACCAGTTCTGGATAAAGTGGGTGAGGCAGAGG 120
 |||||
 Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTAC 180
 |||||
 Sbjct: 121 CCTGGACAAGGCCTTGAGTGGATTGGAAATATTTATCCTGGTAGTAGTAGTATTAACCTAC 180
 |||||
 Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
 |||||
 Sbjct: 181 AATGAGAAGTTCAAGAACAAGGCCACACTGACTGTAGACACATCCTCCAGCACAGCCTAC 240
 |||||
 Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG 297
 |||||
 Sbjct: 241 ATGCAGCTCAGCAGCCTGACATCTGACGACTCTGCGGTCTATTATTGTGCAAGACGG 297
 |||||

Score = 221 (61.1 bits), Expect = 3.2e-101, Sum P(2) = 3.2e-101
 Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360
 |||||

>emb|Z12765|MM37F2A M.musculus mRNA for VH-gen sequence of naturally occurring,
 somatically mutated memory B cell
 Length = 363

Plus Strand HSPs:

Score = 1086 (300.1 bits), Expect = 3.9e-101, Sum P(2) = 3.9e-101
 Identities = 258/309 (83%), Positives = 258/309 (83%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
 |||||
 Sbjct: 1 CAGGTCCAACCTGCAGCAGCCTGGGGCTGAGCTGGTGAGGCCTGGGTCTCAGTGAAGCTG 60
 |||||

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAGCAGACA 120
 |||||
 Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTACCAGCTACTGGATGCATTGGGTGAAGCAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
 |||||
 Sbjct: 121 CCTATACAAGGCCTTGAATGGATTGGTAACATTGACCCTTCTGATAGTAACTCACTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
 |||||
 Sbjct: 181 AATCAAAAGTTCAAGGACAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 300
 |||||
 Sbjct: 241 ATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGAGAGC 300

Query: 301 TGGGAGGGT 309
 |||||
 Sbjct: 301 TACTATGGT 309

Score = 205 (56.6 bits), Expect = 3.9e-101, Sum P(2) = 3.9e-101
 Identities = 45/50 (90%), Positives = 45/50 (90%), Strand = Plus / Plus

Query: 305 AGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 314 ACGGGGCTATGGACTACTGGGGCCAGGGAACCTCAGTCACCGTCTCCTCA 363

>gb|U10410|MMU10410 Mus musculus recombinant antineuraminidase single chain Ig
 VH and VL domains mRNA, complete cds.
 Length = 831

Plus Strand HSPs:

Score = 1191 (329.1 bits), Expect = 4.7e-101, Sum P(2) = 4.7e-101
 Identities = 263/294 (89%), Positives = 263/294 (89%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
 |||||
 Sbjct: 67 CAGGTGCAGCTGCAGCAGTCTGGGGCTGAACTGGTGAAGCCTGGGGCCTCAGTGAGGATG 126

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAGCAGACA 120
 |||||
 Sbjct: 127 TCCTGCAAGGCTTCTGGCTACACATTTACCAATTACAACATGTACTGGGTAACACAGTCA 186

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
 |||||
 Sbjct: 187 CCTGGACAGGGCCTGGAGTGGATTGGAATTTTATCCAGGAAATGGTGATACTTCCTAC 246

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
 |||||
 Sbjct: 247 AATCAGAAGTTCAAAGACAAGGCCACATTGACTGCTGACAAATCCTCCAACACAGCCTAC 306

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294
 |||||
 Sbjct: 307 ATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 360

Score = 150 (41.4 bits), Expect = 4.7e-101, Sum P(2) = 4.7e-101
 Identities = 38/48 (79%), Positives = 38/48 (79%), Strand = Plus / Plus

Query: 304 GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 351
 |||||
 Sbjct: 382 GACGGAGGCTTTGACTACTGGGGCAAGGGACCACGGTCACCGTCTCC 429

>gb|M32036|MUSIGHRJ Mouse Ig H-chain mRNA V-D-J region, from hybridoma P65D6-3,
 partial cds.
 Length = 363

Plus Strand HSPs:

Score = 1146 (316.7 bits), Expect = 6.8e-101, Sum P(2) = 6.8e-101
Identities = 270/321 (84%), Positives = 270/321 (84%), Strand = Plus / Plus

```

Query:      2 AGGCTTATCTACAGCAGCTCTGGGGCTGAGCTGGTGAGGTCTGGGGCTCAGTGAAGATGT 61
             ||| | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:      2 AGGTTCAAGCTTCAGCAGCTCTGGAGCTGAGCTGGTGAGGGCTGGGTCTCAGTGAAGATGT 61

Query:      62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:      62 CCTGCAAGGCTTCTGGATATACATTACAAGCTACGGTATAAACTGGGTGAAACAGAGGC 121

Query:      122 CTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTACA 181
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:      122 CTGGACAGGGCCTGGAATGGATTGGAATATTTAATCTGGAAATGGTTATACTAAGTACA 181

Query:      182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      182 ATGAGAAGTTCAAGGGCAAGACCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACA 241

Query:      242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGA 301
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:      242 TGCAGCTCAGAAGCCTGACATCTGAGGACTCTGCAGTCTATTTCTGTGCAAGATCCCATT 301

Query:      302 GGGAGGGTGCTCTGGACTACT 322
             ||||| ||||| ||||| |||||
Sbjct:      302 ACTATGGTGGTAGCTACTACT 322

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Score = 142 (39.2 bits), Expect = 6.8e-101, Sum P(2) = 6.8e-101
Identities = 34/41 (82%), Positives = 34/41 (82%), Strand = Plus / Plus

Query: 314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCCTCTCTCA 354
| | | | | | | | | | | | | | | | | | | | |
Sbjct: 323 TTGACTACTGGGGCCAAGGCCAACCCTCTCACAGTCTCTCTCA 363

>emb|Z68170|MMVAR605 M.musculus mRNA for immunoglobulin heavy chain variable region (clone 605). >emb|Z68170|MMVAR605 M.musculus mRNA for immunoglobulin heavy chain variable region (clone 605)
Length = 363

Plus Strand HSPs:

Score = 1065 (294.3 bits), Expect = 1.0e-100, Sum P(2) = 1.0e-100
Identities = 249/294 (84%), Positives = 249/294 (84%), Strand = Plus / Plus

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Query:      1  CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCTCTGGGGCCTCAGTGAAGATG  60
             |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:      1  CAGGTCAAGCTGCAGCAGTCAGGGACTGTGCTGGCAAGGCCTGGGGCTTCAGTGAAATG  60

Query:     61  TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA  120
             |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:     61  TCCTGCAAGGCTTCTGGCTACAÇTTTACCAGCTACTGGATGCACTGGGTAAAACAGAGG  120

Query:    121  CCTGGACAGGGCCTGGAATGGATTGAAATATTTTTCTGGAAATGGTGATACTTACTAC  180
             |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:    121  CCTGGACAGGGTCTGGAATGGATTGGCGCTATTTATCCTGGAAATAGTGATACTAGCTAC  180

Query:    181  AATCAGAAGTTTAAAGGGCAAGGCCTCATTGACTGCAGACACATCTCCAGCACAGCCTAC  240
             |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:    181  AACCAGAAGTTC AAGGGCAAGGCCAAACTGACTGCAGTCACATCCACCAGCACTGCCTAC  240

Query:    241  ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCCTGTGCAAGA  294
             |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:    241  ATGGAGCTCAGCAGCCTGACAAATGAGGACTCTGCGGTCTATTACTGTACAGA  294

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```

Query:      2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCTCTGGGGCCCTCAGTGAAGATGT 61
             |||
Sbjct:      2 AGGTTCAAGCTTCTGAGCTCTGGAGCTGAGCTGGTGAGGGCTGGGTCTCAGTGAAGATGT 61
             |||

Query:      62 CTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
             |||
Sbjct:      62 CTGCAAGGCTTCTGGATATACATTACAAGCTACGGTATAAACTGGGTGAAACAGAGGC 121
             |||

Query:      122 CTGGACAGGGCCTGGAATGGATTGAAAATATTTTCTCGAAATGGTGATACTTACTACA 181
             |||
Sbjct:      122 CTGGACAGGGCCTGGAATGGATTGGATATATTAATCTCGAAATGGTTATACTAAGTACA 181
             |||

Query:      182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
             |||

```

Sbjct: 182 ATGAGAAGTTCAAGGGCAAGACCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACA 241

Query: 242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGA 301

Sbjct: 242 TGCAGCTCAGAAGCCTGACATCTGAGGAYTCTGCAGTCTATTTCTGCGCAAGATCGGTCT 301

Query: 302 GGGAGGGTGTCTGGACTACT 322

Sbjct: 302 ACTATGGTGGTAGTTACTACT 322

Score = 142 (39.2 bits), Expect = 1.5e-100, Sum P(2) = 1.5e-100
Identities = 34/41 (82%), Positives = 34/41 (82%), Strand = Plus / Plus

Query: 314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 323 TTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 363

>emb|222028|MDIGGVAD M.domesticus IgG variable region.
Length = 363

Plus Strand HSPs:

Score = 1071 (295.9 bits), Expect = 1.8e-100, Sum P(2) = 1.8e-100
Identities = 251/297 (84%), Positives = 251/297 (84%), Strand = Plus / Plus

Query: 2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61

Sbjct: 2 AGGTCCAGCTGCAGCAGTCTGGACCTGAGTTGGTAAAGCCTGGGGCCTCAGTGAAGATGT 61

Query: 62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121

Sbjct: 62 CCTGCAAGGCTTCTGGATACACATTCAGTAGATATGTTATGCACTGGGTAAAGCAGAAGC 121

Query: 122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181

Sbjct: 122 CTGGGCAGGGCCTTGAGTGGATTGGATATATTAATCCTTACAATGATGGTACTAAATACA 181

Query: 182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241

Sbjct: 182 ATGAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGCACAGCCTACA 241

Query: 242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGA 298

Sbjct: 242 TGGAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGGA 298

Score = 212 (58.6 bits), Expect = 1.8e-100, Sum P(2) = 1.8e-100
Identities = 44/46 (95%), Positives = 44/46 (95%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 318 TGCTATGGACTACTGGGGTCAAGGAGCCTCAGTCACCGTCTCCTCA 363

>gb|L24557|MUSIGHMADQ Mus musculus (S03) monoclonal anti-HLA-DQ3 monoclonal
antibody IgH chain mRNA, V-region.
Length = 368

Plus Strand HSPs:

Score = 1051 (290.4 bits), Expect = 3.1e-100, Sum P(2) = 3.1e-100
Identities = 247/293 (84%), Positives = 247/293 (84%), Strand = Plus / Plus

Query: 2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61

Sbjct: 1 AGGTCAAGCTGCAGGAGTCAGGGGCTGAACTGGCAAGACCTGGGGCCTCAGTGAAGATGT 60

Query: 62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121

```

Sbjct: 61 CCTGCAAGGCTTCTGGCTACACCTTTAGTAGGTAAGTGCATGGGTGAAACAGCGGC 120
Query: 122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
Sbjct: 121 CTGGACAGGGTCTGGAATGGATTGGATACATTATCCTACCAGTGTTATACTAATTACA 180
Query: 182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
Sbjct: 181 ATCAGAAGTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACA 240
Query: 242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294
Sbjct: 241 TGCAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA 293

```

Score = 229 (63.3 bits), Expect = 3.1e-100, Sum P(2) = 3.1e-100
Identities = 49/53 (92%), Positives = 49/53 (92%), Strand = Plus / Plus

```

Query: 302 GGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
Sbjct: 316 GGGACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 368

```

>gb|J00493|MUSIGHAP Mouse Ig active H-chain V-region from 93G7, subgroup VH-II,
mRNA.
Length = 437

Plus Strand HSPs:

Score = 1137 (314.2 bits), Expect = 3.2e-100, Sum P(2) = 3.2e-100
Identities = 269/321 (83%), Positives = 269/321 (83%), Strand = Plus / Plus

```

Query: 2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61
Sbjct: 76 AGGTTCAAGCTTCAGCAGTCTGGAGCTGAGCTGGTGAGGGCTGGGTCCTCAGTGAAGATGT 135
Query: 62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
Sbjct: 136 CCTGCAAGGCTTCTGGATATACATTCAAGCTACGGTATAAACTGGGTGAAACAGAGGC 195
Query: 122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
Sbjct: 196 CTGGACAGGGCCTGGAATGGATTGGATATATTAATCCTGGAAATGGTTATATTAACTACA 255
Query: 182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
Sbjct: 256 ATGAGAAGTTCAAGGGCAAGACCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACA 315
Query: 242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAGT 301
Sbjct: 316 TGCAGCTCAGAAGCCTGACATCTGAGGACTCTGCAGTCTATTCTGTGCAAGATCCCAT 375
Query: 302 GGGAGGGTGCTCTGGACTACT 322
Sbjct: 376 ACTATGGTGGTAGCTACGACT 396

```

Score = 142 (39.2 bits), Expect = 3.2e-100, Sum P(2) = 3.2e-100
Identities = 34/41 (82%), Positives = 34/41 (82%), Strand = Plus / Plus

```

Query: 314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
Sbjct: 397 TTGACTACTGGGGCCAAGGCACCCCTCTCACAGTCTCCTCA 437

```

>gb|M32035|MUSIGHRI Mouse Ig H-chain mRNA V-D-J region, from hybridoma P65D6-7,
partial cds.
Length = 363

Query: 314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 320 TTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 360

>emb|222088|MDIGGVAR M.domesticus IgG variable region.
 Length = 357

Plus Strand HSPs:

Score = 1056 (291.8 bits), Expect = 3.9e-100, Sum P(2) = 3.9e-100
 Identities = 248/294 (84%), Positives = 248/294 (84%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGCTGAGCTGGTGAAGTCTGGGCCTCAGTGAAGATG 60
 |||||
 Sbjct: 1 CAGGTCCAGCTGCAGCAGTCAAGGCTGAAGTGGCAAGACCTGGGCCTCAGTGAAGATG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
 |||||
 Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTTACCAGATACTGGATGCACTGGGTAAACAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
 |||||
 Sbjct: 121 CCTGGACAGGCTCTGGAATGGATTGGCGCTATTTATCCTGGAAATAGTGATACTAATAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
 |||||
 Sbjct: 181 AACCAGAAATTCAAGGGCAAGGCCAACTGACTGCAGTCACATCTGCCAGCACTGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294
 |||||
 Sbjct: 241 ATGGAACCTCAGCAGCCTGGCATCTGAGGACTCTGCCGTCTATTACTGTGCAAGA 294

Score = 223 (61.6 bits), Expect = 3.9e-100, Sum P(2) = 3.9e-100
 Identities = 51/59 (86%), Positives = 51/59 (86%), Strand = Plus / Plus

Query: 296 GGAACCTGGGAGGGTGTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 299 GGTACAGGGGATATTCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

>gb|M97876|MUSL77IGHV Mouse hybridoma Ig rearranged H-chain mRNA V-region,
 partial cds.
 Length = 390

Plus Strand HSPs:

Score = 1066 (294.6 bits), Expect = 4.3e-100, Sum P(2) = 4.3e-100
 Identities = 246/287 (85%), Positives = 246/287 (85%), Strand = Plus / Plus

Query: 8 ATCTACAGCAGTCTGGGCTGAGCTGGTGAAGTCTGGGCCTCAGTGAAGATGTCCTGCA 67
 |||||
 Sbjct: 8 ATCTTCAGGAGTCGGGACCTGAGCTGGTGAAGCCTGGGCTTCAAGTGAAGATGTCCTGCA 67

Query: 68 AGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGAC 127
 |||||
 Sbjct: 68 AGGCTTCTGGATACACATTCACTGACTATGTTATAACCTGGGTGAAGCCGAGAAGTGGAC 127

Query: 128 AGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTACAATCAGA 187
 |||||
 Sbjct: 128 AGGGCCTTGAGTGGATTGGAGAGATTATCCTGGAAGTGGTAGTGCTTACTACAATGAGA 187

Query: 188 AGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGA 247
 |||||
 Sbjct: 188 AGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAACACAGCCTACATGCAGC 247

Query: 248 TCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294

Sbjct: 248 TCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGA 294

Score = 212 (58.6 bits), Expect = 4.3e-100, Sum P(2) = 4.3e-100
Identities = 44/46 (95%), Positives = 44/46 (95%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 315 TGCCTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

>gb|M61026|MUSIGHAANN M.musculus Ig rearranged H-chain mRNA V-D-J-region,
partial cds.
Length = 354

Plus Strand HSPs:

Score = 1266 (349.8 bits), Expect = 4.4e-100, P = 4.4e-100
Identities = 298/354 (84%), Positives = 298/354 (84%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60

Sbjct: 1 CAGGTCCAACCTGCAGCAGCCTGGGGCTGAGCTTGGAAGCCTGGGGCTTCAGTGAAGCTG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120

Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTCACCAGTACTTGATGCACTGGGTGAAGCAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180

Sbjct: 121 CCTGGACAGGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCCTATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240

Sbjct: 181 AATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAACCTCCAGCACAGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 300

Sbjct: 241 ATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGCAAGATATTAC 300

Query: 301 TGGGAGGGTGTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 301 TACGGTGGTGTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

>emb|Z12794|MMV20552B M.musculus mRNA for VH-gen sequence of naturally
occurring, somatically mutated memory B cell
Length = 369

Plus Strand HSPs:

Score = 1057 (292.1 bits), Expect = 4.5e-100, Sum P(2) = 4.5e-100
Identities = 253/305 (82%), Positives = 253/305 (82%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60

Sbjct: 1 CAGGTCCAACCTGCAGCAGCCTGGGGCTGAACCTTGGAAGCCTGGGGCTTCAGTGAAGCTG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120

Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTCACCAGTACTGGATGCACTGGGTAAAGCAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180

Sbjct: 121 CCTGGACAGGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCCTATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240

|||||

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Sbjct: 181 AATGAGAAGTTCAAGAGCAAGGCCACTGACTGTAGACAAACCTCCAGCACAGCCTAC 240
Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 241 ATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGCAAGAGACTAC 300
Query: 301 TGGGA 305
      |  ||
Sbjct: 301 TATGA 305

```

Score = 221 (61.1 bits), Expect = 4.5e-100, Sum P(2) = 4.5e-100
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||
 Sbjct: 324 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 369

>emb|Z12799|MHV20652B M.musculus mRNA for VH-gen sequence of naturally occurring, somatically mutated memory B cell
Length = 369

Plus Strand HSPs:

Score = 1057 (292.1 bits), Expect = 4.5e-100, Sum P(2) = 4.5e-100
Identities = 253/305 (82%), Positives = 253/305 (82%), Strand = Plus / Plus

```
Query:      1 CAGGCTATCTACAGCAGCTG GGGCTGAGCTGGTGAAGTCTGGGGCCTCAGTGAAGATG   60
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     1 CAGGTCCAAC TGCAGCAGCTGGGGCTGAGCTTG TGAAGCCTGGGGCTTCAGTGAAGCTG   60

Query:    61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCATGGGTAAAGCAGACA   120
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    61 TCCTGCAAGGCTTCTGGCTACACCTTACCAGCTACTGGATGCATGGGTGAAGCAGAGG   120

Query:    121 CCTGGACAGGGCCTGGAATGGATTGAAATATTTTTCTGGAAATGGTGATACTTACTAC   180
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    121 CCTGGACAGGCCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTAC   180

Query:    181 AATCAGAAGTTTAAGGGCAAGGCCTATTGACTGCAGACACATCCTCCAGCACAGCCTAC   240
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    181 AATGAGAAGTTCAAGAGCAAGGCCACTGACTGTAGACAAACCTCCAGCACAGCCTAC   240

Query:    241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC   300
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    241 ATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGCAAGAGACTAC   300

Query:    301 TGGA 305
           ||
Sbjct:    301 TATGA 305
```

Score = 221 (61.1 bits), Expect = 4.5e-100, Sum P(2) = 4.5e-100
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

```
Query:   309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA    354
          ||| ||||| ||||||||| ||||||| |
Sbjct:   324 TGCTATGGAATACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA    369
```

```
>emb|Z22129|MD1GMVBC M.domesticus IgM variable region.  
Length = 363
```

Plus Strand HSPs:

Score = 1057 (292.1 bits), Expect = 4.6e-100, Sum P(2) = 4.6e-100
Identities = 249/296 (84%), Positives = 249/296 (84%), Strand = Plus / Plus

Query: 2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61

```

Sbjct:      2 AGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGT 61
Query:      62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
Sbjct:      62 CCTGCAAGGCTTCTGGATACACATTCAGTATGTTATGCACTGGGTGAAGCAGAAGC 121
Query:     122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
Sbjct:     122 CTGGGCAGGGCCTTGAGTGGATTGGATATATTAATCCTTACAATGATGGTACTAAGTACA 181
Query:     182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
Sbjct:     182 ATGAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGCACAGCCTACA 241
Query:     242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG 297
Sbjct:     242 TGGAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTACTGTGCAAGAAGG 297

```

Score = 221 (61.1 bits), Expect = 4.6e-100, Sum P(2) = 4.6e-100
 Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

```

Query:     309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
Sbjct:     318 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 363

```

>emb|222134|MDIGMVB M.domesticus IgM variable region.
 Length = 363

Plus Strand HSPs:

Score = 1063 (293.7 bits), Expect = 8.2e-100, Sum P(2) = 8.2e-100
 Identities = 255/308 (82%), Positives = 255/308 (82%), Strand = Plus / Plus

```

Query:      2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAAGTCTGGGGCCTCAGTGAAGATGT 61
Sbjct:      2 AGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGT 61
Query:     62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
Sbjct:     62 CCTGCAAGGCTTCTGGATACACATTCAGTATGTTATGCACTGGGTGAAGCAGAAGC 121
Query:    122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
Sbjct:    122 CTGGGCAGGGCCTTGAGTGGATTGGATATATTAATCCTTACAATGATGGTACTAAGTACA 181
Query:    182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
Sbjct:    182 ATGAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGCACAGCCTACA 241
Query:    242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAGT 301
Sbjct:    242 TGGAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTACTGTGCAAGGGGGGCC 301
Query:    302 GGGAGGGT 309
Sbjct:    302 GGTATGAT 309

```

Score = 212 (58.6 bits), Expect = 8.2e-100, Sum P(2) = 8.2e-100
 Identities = 44/46 (95%), Positives = 44/46 (95%), Strand = Plus / Plus

```

Query:     309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
Sbjct:     318 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 363

```

>gb|M64141|MUSIGHNOL Mouse Ig active heavy-chain mRNA V-region.

Length = 339

Plus Strand HSPs:

Score = 1046 (289.0 bits), Expect = 8.8e-100, Sum P(2) = 8.8e-100
Identities = 242/283 (85%), Positives = 242/283 (85%), Strand = Plus / Plus

```
Query:      15 GCAGCTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCC 74
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      1  GCAGCTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGTCCTGCAAGGCC 60

Query:     75 TGGCTACACATTGACCAGTTACAATATGCAGCTGGGTAAGCAGACACCTGGACAGGGCCT 134
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     61 TGGATACACATTCACTAGCTATGTTATGCAGCTGGGTGAAGCAGAAGCCTGGGCAGGGCT 120

Query:    135 GGAATGGATTGGAATAATTTTTCTGGAAATGGTGACTTACTACAATCAGAAGTTTAA 194
             ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    121 TGAGTGGATTGGATATATTAATCCTTACAATGATGGTACTAAGTACAATGAGAAGTTCAA 180

Query:    195 GGGCAAGGCCTCATTTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGATCAGCAG 254
             ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    181 AGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGCACAGCCTACATGGAGCTCAGCAG 240

Query:    255 CCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGG 297
             ||| | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    241 CCTGACCTCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGG 283
```

Score = 229 (63.3 bits), Expect = 8.8e-100, Sum P(2) = 8.8e-100
Identities = 49/53 (92%), Positives = 49/53 (92%), Strand = Plus / Plus

Query: 302 GGGAGGGTCTCTGGACTACTGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
||| ||| |
Sbjct: 282 GGGGGGATGGTATGGAATACTGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 334

>gb|109505|109505 Sequence 3 from patent WO 8909622.
Length = 443

Plus Strand HSPs:

Score = 1107 (305.9 bits), Expect = 9.8e-100, Sum P(2) = 9.8e-100
Identities = 255/297 (85%), Positives = 255/297 (85%), Strand = Plus / Plus

```

Query:      1  CAGGCTTATCTACAGCAGCTCTGGGGCTGAGCTGGTGAGGCTCTGGGGCCTCAGTGAAGATG  60
             |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:     95  CAGGTCACAGCTTCAGCAGCTCTGGGGCTGAACGGCAAAACCTGGGGCCTCAGTGAAGATG  154

Query:     61  TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAGCAGACA  120
             |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:    155  TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACAGGATGCACTGGGTAAGCAGAGG  214

Query:    121  CCTGGACAGGGCCTGGAATGGATTGAAATATTTTCTGGAAATGGTGATACTTACTAC  180
             |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:    215  CCTGGACAGGGTCTGGAATGGATTGGATATATTAATCCTAGCACTGGGTATACTGAATAC  274

Query:    181  AATCAGAAGTTTAAGGGCAAGGCCCTATTGACTGCAGACACATCCTCCAGCACAGCCTAC  240
             |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:    275  AATCAGAAGTTCAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC  334

Query:    241  ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGG  297
             |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:    335  ATGCAACTGAGCAGCCTGACATTTGAGGACTCTGCAGCTCTATTACTGTGCAAGAGGG  391

```

Score = 166 (45.9 bits), Expect = 9.8e-100, Sum P(2) = 9.8e-100
Identities = 42/53 (79%), Positives = 42/53 (79%), Strand = Plus / Plus

Query: 302 GGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
||||| | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 390 GGGGGGGGCTCTTTGACTACTGGGGCCAAGGAACCACTCTCACAGTCTCCTCA 442

>gb|M31908|MUSIGHRC Mouse Ig H-chain V-D-J region mRNA, from hybridoma
hVH65-211, partial cds.
Length = 363

Plus Strand HSPs:

Score = 1132 (312.8 bits), Expect = 9.9e-100, Sum P(2) = 9.9e-100
Identities = 264/311 (84%), Positives = 264/311 (84%), Strand = Plus / Plus

```

Query:      2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61
            |||||
Sbjct:      2 AGGTTCAGCTTCAGCAGTCTGGAGCTGAGCTGGTGAGGGCTGGGTCTCAGTGAAGATGT 61

Query:     62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
            |||||
Sbjct:     62 CCTGCAAGGCTTCTGGATATACATTACAAGCTACGGTATAAACTGGGTGAAACAGAGGC 121

Query:    122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
            |||||
Sbjct:    122 CTGGACAGGGCCTGGAATGGATTGGATATATTAATCCTGGAAATGGTTATATTAAGTACA 181

Query:    182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
            |||||
Sbjct:    182 ATGAGAAGTTCAAGGGCAAGACCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACA 241

Query:    242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 301
            |||||
Sbjct:    242 TGCAGCTCAGAAGCCTGACATCTGAGGACTCTGCAGTCTATTTCTGTGCAAGATCGGAAT 301

Query:    302 GGGAGGGTGCT 312
            |||||
Sbjct:    302 ACTATGGTGGT 312

```

Score = 142 (39.2 bits), Expect = 9.9e-100, Sum P(2) = 9.9e-100
Identities = 34/41 (82%), Positives = 34/41 (82%), Strand = Plus / Plus

```

Query:    314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
            |||||
Sbjct:    323 TTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 363

```

>gb|M28251|MUSIGHMX Mouse Ig rearranged gamma-chain (G-2a) mRNA V-region
(V-J2), partial cds.
Length = 406

Plus Strand HSPs:

Score = 1107 (305.9 bits), Expect = 1.1e-99, Sum P(2) = 1.1e-99
Identities = 255/297 (85%), Positives = 255/297 (85%), Strand = Plus / Plus

```

Query:      1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
            |||||
Sbjct:     58 CAGGTCCAGCTTCAGCAGTCTGGGGCTGAACCTGGCAAACTGGGGCCTCAGTGAAGATG 117

Query:     61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
            |||||
Sbjct:    118 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACAGGATGCACTGGGTAAACAGAGG 177

Query:    121 CCTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTAC 180
            |||||
Sbjct:    178 CCTGGACAGGGTCTGGAATGGATTGGATATATTAATCCTAGCACTGGGTATACTGAATAC 237

Query:    181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
            |||||
Sbjct:    238 AATCAGAAGTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC 297

```

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCGTGCAAGAGGG 297
||||| | ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 298 ATGCAACTGAGCAGCCTGACATTTGAGGACTCTGCAGTCTATTACTGTGCAAGAGGG 354

Sbjct: 121 CCTGGACATGGCCTTGAGTGGATTGGAGATATTTACCCTGGAGGTGGTTATACTAACTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240

Sbjct: 181 AATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACACATCCTCCAGCACAGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAG 293

Sbjct: 241 ATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCCATCTATTACTGTGCAAG 293

Score = 213 (58.9 bits), Expect = 1.2e-99, Sum P(2) = 1.2e-99
Identities = 49/57 (85%), Positives = 49/57 (85%), Strand = Plus / Plus

Query: 295 GGGAACTGGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 351

Sbjct: 298 GGGTATGGTTACGTTGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 354

>emb|A23297|A23297 M.musculus CTM01 monoclonal antibody gene, variable domain
of heavy chain
Length = 416

Plus Strand HSPs:

Score = 1073 (296.5 bits), Expect = 1.5e-99, Sum P(2) = 1.5e-99
Identities = 249/292 (85%), Positives = 249/292 (85%), Strand = Plus / Plus

Query: 8 ATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGCTCTGCA 67

Sbjct: 65 AGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTCAGTGAAGATATCCTGCA 124

Query: 68 AGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGAC 127

Sbjct: 125 AGGCTTCTGGCTACACCTTCACTGACTACTATATAAAGTGGATGAAGCAGAAGCCTGGAC 184

Query: 128 AGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTACAATCAGA 187

Sbjct: 185 AGGCACTTGAGTGGATTGGATGGATTGATCCTGGAAGCGGTAATACTAAGTACAATGAGA 244

Query: 188 AGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGA 247

Sbjct: 245 AGTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCTCCAGCACAGCCTACATGCAGC 304

Query: 248 TCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAA 299

Sbjct: 305 TCAGCAGCCTGACATCTGAGGACACTGCTGTCTATTTCTGTGCAAGAGAGAA 356

Score = 198 (54.7 bits), Expect = 1.5e-99, Sum P(2) = 1.5e-99
Identities = 42/45 (93%), Positives = 42/45 (93%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTC 353

Sbjct: 372 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACTGTCTCCGC 416

>emb|Z12798|MMV20642B M.musculus mRNA for VH-gen sequence of naturally
occurring, somatically mutated memory B cell
Length = 369

Plus Strand HSPs:

Score = 1048 (289.6 bits), Expect = 2.5e-99, Sum P(2) = 2.5e-99
Identities = 252/305 (82%), Positives = 252/305 (82%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60

Sbjct: 1 CAGGTCCAACCTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAAGTGAAGCTG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
 |||||
 Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTACCAGCTACTGGATGCACTGGGTGAAGCAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
 |||||
 Sbjct: 121 CCTGGACAGGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
 |||||
 Sbjct: 181 AATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAACCTCCAGCACAGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGGAAC 300
 |||||
 Sbjct: 241 ATGCAGCTCAGCAGCCTGACACCTGAGGACTCTGCGGTCTATTATTGTGCAAGAGACTAC 300

Query: 301 TGGGA 305
 ||
 Sbjct: 301 TATGA 305

Score = 221 (61.1 bits), Expect = 2.5e-99, Sum P(2) = 2.5e-99
 Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 324 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 369

WARNING: HSPs involving 4964 database sequences were not reported due to the limiting value of parameter B = 50.

Parameters:

V=100
 B=50
 H=1
 -qtype
 E=10

-ctxfactor=2.00

Query	Strand	MatID	Matrix name	----- Lambda	As Used K	----- H	----- Lambda	Computed K	----- H
+1	0	+5,-4	0.192	0.173	0.357	same	same	same	
-1	0	+5,-4	0.192	0.173	0.357	same	same	same	

Query	Strand	MatID	Length	Eff.Length	E	S	W	T	X	E2	S2
+1	0		354	354	10.117	11	N/A	73	0.025	76	
-1	0		354	354	10.117	11	N/A	73	0.025	76	

Statistics:

Query	Strand	MatID	Expected High Score	Observed High Score	HSPs Reportable	HSPs Reported
+1	0		124 (34.3 bits)	1473 (407.0 bits)	6865	93
-1	0		124 (34.3 bits)	1065 (294.3 bits)	31	0

Query	Strand	MatID	Neighborhd Words	Word Hits	Excluded Hits	Failed Extensions	Successful Extensions	Overlaps Excluded
+1	0		347	86244	31541	44804	9985	378
-1	0		347	48074	4289	42064	1816	1

Database: Non-redundant PDB+GBupdate+GenBank+EMBLupdate+EMBL

Release date: 6:31 AM EST Jan 19, 1996

Posted date: 6:39 AM EST Jan 19, 1996

of letters in database: 449,479,361

of sequences in database: 662,343

of database sequences satisfying E: 5014

No. of states in DFA: 204 (204 KB)

Total size of DFA: 213 KB (256 KB)
Time to generate neighborhood: 0.02u 0.01s 0.03t Real: 00:00:00
No. of processors used: 3
Time to search database: 30.08u 3.42s 33.50t Real: 00:01:10
Total cpu time: 30.22u 3.54s 33.76t Real: 00:01:11

WARNINGS ISSUED: 2

S. Chatterjee

===== 1382

Return-Path: <blastmai@BLASTER.NLM.NIH.GOV>

Received: from UKCC (NJE origin SMTP@UKCC) by UKCC.UKY.EDU (LMail V1.2a/1.8a) with BSMTTP id 2504; Fri, 19 Jan 1996 17:18:47 -0500

Received: from ncbi.nlm.nih.gov by UKCC.uky.edu (IBM VM SMTP V2R3) with TCP; Fri, 19 Jan 96 17:18:44 EST

Received: from blaster.nlm.nih.gov by ncbi.nlm.nih.gov id RAA28107; Fri, 19 Jan 1996 17:18:34 -0500

Received: by blaster.nlm.nih.gov (950511.SGI.8.6.12.PATCH526/5.6) id RAA05609; Fri, 19 Jan 1996 17:18:33 -0500

Date: Fri, 19 Jan 1996 17:18:33 -0500

Message-Id: <199601192218.RAA05609@blaster.nlm.nih.gov>

To: SKCHAT00@UKCC.uky.edu

Subject: Results-BLAST Server

From: NCBI BLAST E-Mail Server <blast@ncbi.nlm.nih.gov>

Errors-To: <owner-blast@ncbi.nlm.nih.gov>

Reply-To: "NCBI BLAST E-Mail Server" <blast@ncbi.nlm.nih.gov>

--+=====

To Obtain Documentation: send an e-mail message to 'blast@ncbi.nlm.nih.gov' with the word HELP in the body of the message. The documentation was last modified March 18th.

--+=====

March 18, 1995

The BLAST FAQ was updated with the question Q33 related to degenerated nucleotide code available for the BLAST programs.

August 8, 1995

A new server directive ACKNOWLEDGE, has been added to the server. See the help file for more details.

--+=====

Trying blaster... connected

National Center for Biotechnology Information (NCBI)

Experimental GENINFO(R) BLAST Network Service (Blaster)

Fri Jan 19 17:17:34 EST 1996, Up 30 days, 5:08, 1 user, load: 62.31, 41.55, 28.47

PEPTIDE SEQUENCE DATABASES

nr Non-redundant PDB+SwissProt+PIR+SPUpdate+GenPept+GPUpdate, updated daily for efficient, complete searches of the five component databases:

pdb Brookhaven Protein Data Bank, April 1995 Release

swissprot SWISS-PROT Release 32.0, December 1995

pir PIR Release 45.0 (complete), June 30, 1995

spupdate SWISS-PROT cumulative weekly update to the major release

genpept CDS translations from GenBank(R) Release 92, December 15, 1995

gpupdate cumulative daily updates to the major release of genpept

kabatpro Kabat Sequences of Proteins of Immunological Interest, June 1995

tfd TFD transcription factor (protein) database Release 7.0, June 1993

alu * Translations of select Alu repeats from REPBASE

NUCLEOTIDE SEQUENCE DATABASES

nr Non-redundant PDB+GBUpdate+GenBank+EmblUpdate+EMBL, updated daily for efficient, complete searches of the four component databases:

pdb Brookhaven Protein Data Bank, April 1995 Release

genbank GenBank(R) Release 92 (no daily updates), December 15, 1995

gbupdate GenBank(R) cumulative daily updates to the major release

embl EMBL Data Library, Release 45.0, December 1995

emblu EMBL Data Library cumulative daily updates to the major release

vector Vector subset of GenBank(R), February 3rd, 1995

alu ** Select Alu repeats from REPBASE

kabatnuc Kabat Sequences of Nucleic Acid of Immunological Interest, June 1995

epd Eukaryotic Promoter Database Release 43, June 1995

dbest + Database of Expressed Sequence Tags (cumulative daily update)

dbsts + Database of Sequence Tagged Sites Release 1.5, October 26, 1994

* Databases that are not accessible through the NCBI Retrieve E-mail server.
+ The TBLASTX program is restricted to searching these databases.

You can obtain the BLAST documentation files, send a message consisting of just the word ``help'' (without the quotes) to: blast@ncbi.nlm.nih.gov
Last modification dates: August 10th 95 for the E-mail server help, January 19th 94 for the BLAST manual and March 18th 95 for the BLAST FAQ.

For a free subscription to "NCBI News", the NCBI newsletter, send a request along with your name and postal mailing address to: info@ncbi.nlm.nih.gov

A new GenBank sequence submission tool, called BankIt, is now available through the NCBI's home page on the World Wide Web. The URL is <http://www.ncbi.nlm.nih.gov/>

BLASTP 1.4.8MP [20-June-1995] [Build 13:58:02 Oct 17 1995]

Reference: Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Query= 11D10VH.pep
(118 letters)

Database: Non-redundant PDB+SwissProt+SPupdate+PIR+GenPept+GPupdate
172,206 sequences; 51,001,589 total letters.

Searching.....done

Observed Numbers of Database Sequences Satisfying
Various EXPECTation Thresholds (E parameter values)

Histogram units: = 39 Sequences : less than 39 sequences

**EXPECTation Threshold
(E parameter)**

[illegible]

```

0.016 6047 117 ===
0.010 5930 75  =
0.0063 5855 98  ==
0.0040 5757 112 ==
0.0025 5645 104 ==
0.0016 5541 72  =

```

Sequences producing High-scoring Segment Pairs:			High Score	Smallest Sum Probability P(N)	N
gp X64805 MMAIDHCH_1	anti-Id mAb 114 haevy chain, V-reg...	542	7.4e-70	1	
gp M17953 MUSIGHXW_1	immunoglobulin heavy chain [Mus mu...	462	4.2e-65	2	
gp Z22117 MDIGGVBC_1	immunoglobulin variable region [Mu...	430	2.3e-64	2	
gp U10410 MMU10410_1	antineuraminidase single chain ant...	425	1.3e-63	2	
pir S38950 S38950	Ig gamma chain - mouse	420	2.6e-63	2	
gp Z22034 MDIGGVAG_1	immunoglobulin variable region [Mu...	421	4.0e-63	2	
gp U40581 MMU40581_1	sFv antibody [Mus musculus]	409	1.1e-61	2	
gp A13735 A13735_1	V region monoclonal antibody,cross...	390	1.3e-61	2	
pir PS0024 PS0024	Ig heavy chain precursor V region ...	390	1.5e-61	2	
gp Z22059 MDIGGVAN_1	immunoglobulin variable region [Mu...	417	1.7e-61	2	
pir E48677 E48677	Ig heavy chain V-D-J region (48) - ...	404	3.1e-61	2	
gp M32037 MUSIGHRK_1	Mouse Ig H-chain mRNA V-D-J region...	419	3.1e-61	2	
pir S41394 S41394	Ig heavy chain V region - mouse	407	8.1e-61	2	
gp S69279 S69279_1	anti-louping ill virus antibody 4....	405	8.1e-61	2	
gp Z22088 MDIGGVAR_1	immunoglobulin variable region [Mu...	407	8.1e-61	2	
pir F48677 F48677	Ig heavy chain V-D-J region (44.1)...	400	1.1e-60	2	
gp L22747 MUSF_1	immunoglobulin heavy chain [Mus mu...	475	1.1e-60	1	
gp M32036 MUSIGHRJ_1	Mouse Ig H-chain mRNA V-D-J region...	414	1.5e-60	2	
pir A26405 A26405	Ig heavy chain V region (3D10) - m...	400	1.5e-60	2	
gp U26991 MMU26991_1	Ig variable region [Mus musculus]	473	1.8e-60	1	
pir PL0208 PL0208	anti-idiotypic antibody E225, gamm...	418	1.8e-60	2	
gp X53637 MME225H_1	E225 gene product [Mus musculus]	418	1.8e-60	2	
gp M34581 MUSIGHABU_1	Mouse Ig heavy-chain mRNA V-D-J re...	408	2.0e-60	2	
gp L24557 MUSIGHMADQ_1	immunoglobulin heavy chain [Mus mu...	401	2.0e-60	2	
gp M36210 MUSIGHADQ_1	immunoglobulin heavy chain V-regio...	422	2.1e-60	2	
gp M28251 MUSIGHMX_1	Mouse Ig rearranged gamma-chain (G...	406	2.5e-60	2	
gp Z22129 MDIGMVBC_1	immunoglobulin variable region [Mu...	400	2.8e-60	2	
pir S26309 S26309	Ig heavy chain V region - mouse	394	2.9e-60	2	
gp M32035 MUSIGHRI_1	Mouse Ig H-chain mRNA V-D-J region...	411	3.8e-60	2	
gp S74051 S74051_1	Ig VH gene product [Mus sp.]	471	4.0e-60	1	
pir PH1482 PH1482	Ig heavy chain V region (clones 36...	410	4.5e-60	2	
gp X06110 MMIGVHD1_1	Mouse mRNA (36-35) for immunoglobu...	410	5.2e-60	2	
gp Z22134 MDIGMVBF_1	immunoglobulin variable region [Mu...	401	5.2e-60	2	
gp K00684 MUSIGHBG_1	Mouse Ig active H-chain V-region f...	409	6.2e-60	2	
sp P01747 HV03_MOUSE	IG HEAVY CHAIN V REGION (36-65).	409	7.2e-60	2	
pir B22769 B22769	Ig heavy chain V region (B1-8.V1/V...	409	7.2e-60	2	
gp M36216 MUSIGHADW_1	immunoglobulin heavy chain V-regio...	409	7.2e-60	2	
gp L25855 MUSIGGB_1	IgG gene product [Mus musculus]	407	7.3e-60	2	
gp S77022 S77022_1	anti-CD29 antibody heavy chain var...	403	7.5e-60	2	
gp M36225 MUSIGHAEF_1	immunoglobulin heavy chain V-regio...	468	9.9e-60	1	
pir S40295 S40295	Ig gamma-2a chain (mAb735) - mouse	420	1.1e-59	2	
gp L22749 MUSI_1	immunoglobulin heavy chain [Mus mu...	467	1.4e-59	1	
gp M61026 MUSIGHAANN_1	immunoglobulin heavy chain VDJ reg...	467	1.4e-59	1	
gp M31287 MUSIGHAVA_1	IgG gene product [Mus musculus]	466	1.9e-59	1	
gp M31288 MUSIGHAWA_1	Mouse active rheumatoid factor IgA...	466	1.9e-59	1	
gp M31908 MUSIGHRC_1	Mouse Ig H-chain V-D-J region mRNA...	404	2.5e-59	2	
gp M36226 MUSIGHAEG_1	immunoglobulin heavy chain V-regio...	414	2.5e-59	2	
gp U36491 MMU36491_1	J558+ IgM heavy chain [Mus musculus]	402	2.8e-59	2	
gp L35315 MUSIVDJA_1	immunoglobulin heavy chain [Mus mu...	404	2.9e-59	2	
gp X88902 MMVARHECH_1	Fv fragment variable heavy chain [...]	389	3.2e-59	2	
gp M36209 MUSIGHADP_1	immunoglobulin heavy chain V-regio...	415	3.4e-59	2	
gp M12809 MUSIGHJA_1	Mouse Ig rearranged H-chain V-regi...	403	3.4e-59	2	
gp X75095 MMHCVR1_1	ASW1 heavy chain variable regions...	404	3.5e-59	2	
gp M36224 MUSIGHAEE_1	immunoglobulin heavy chain V-regio...	464	3.5e-59	1	
pir A54378 A54378	anti-triplex DNA immunoglobulin he...	464	3.6e-59	1	
sp P01746 HV02_MOUSE	IG HEAVY CHAIN PRECURSOR V REGION ...	405	4.0e-59	2	

pir S21810 S21810	Ig heavy chain V region - mouse >g...	410	4.1e-59	2
gp M33856 MUSIGHABM_1	Mouse Ig H-chain mRNA V-region, 5'...	403	4.2e-59	2
pir G48677 G48677	Ig heavy chain V-D-J region (419.1...	388	4.6e-59	2
gp Z22028 MDIGGVAD_1	Immunoglobulin Variable Region [Mu...	396	4.7e-59	2
gp Z22101 MDIGGVAV_1	immunoglobulin variable region [Mu...	399	4.8e-59	2
pdb 1FBI H	Fab Fragment Of The Monoclonal Ant...	383	6.6e-59	2
gp M31913 MUSIGHRE_1	Mouse Ig H-chain V-D-J region mRNA...	404	8.8e-59	2
gp U39781 MMU39781_1	J558+ IgM heavy chain [Mus musculus]	389	9.4e-59	2
gp M83098 MUSIGHM195_1	immunoglobulin heavy chain [Mus mu...	388	1.1e-58	2
gp M94153 MUSIGKXE_1	immunoglobulin gamma-chain [Mus mu...	400	1.1e-58	2
gp U00927 U00927_1	antibody heavy chain FAB [Mus musc...	386	1.2e-58	2
gp J04548 MUSIGHVBE_1	immunoglobulin gamma-chain [Mus mu...	399	1.4e-58	2
pir PH1489 PH1489	Ig heavy chain V region (clone X41...	399	1.4e-58	2
gp M36213 MUSIGHADT_1	immunoglobulin heavy chain V-regio...	410	1.7e-58	2
gp M36219 MUSIGHADZ_1	immunoglobulin heavy chain V-regio...	404	1.7e-58	2
gp L22746 MUSE_1	immunoglobulin heavy chain [Mus mu...	408	1.7e-58	2
gp M64141 MUSIGHNOL_1	Ig heavy chain [Mus musculus]	391	1.8e-58	2
gp X65773 MLLB4IHEV_1	IgE antibody heavy chain (VDJ) [Mu...	458	2.0e-58	1
pir A30577 A30577	Ig heavy chain precursor V region ...	402	2.7e-58	2
pir S31930 S31930	Ig gamma chain - Mouse (fragment) ...	385	2.9e-58	2
pir S20646 S20646	Ig heavy chain V region - mouse >g...	385	3.0e-58	2
gp M36207 MUSIGHAFR_1	immunoglobulin heavy chain V-regio...	408	3.1e-58	2
gp Z22099 MDIGGVAV_1	immunoglobulin variable region [Mu...	397	3.1e-58	2
gp U23046 MMU23046_1	anti-ds-DNA immunoglobulin heavy c...	385	3.1e-58	2
gp L41877 MUSIHCB_1	immunoglobulin heavy chain [Mus mu...	407	3.7e-58	2
gp U22903 MMU22903_1	IgG Vh region [Mus musculus]	393	4.0e-58	2
pir A21854 A21854	Ig heavy chain V region (IF6) - mouse	382	4.2e-58	2
gp M31281 MUSIGHAPAA_1	Mouse active rheumatoid factor IgA...	392	4.3e-58	2
gp J04547 MUSIGHVBD_1	immunoglobulin gamma-chain [Mus mu...	394	4.8e-58	2
pir S20643 S20643	Ig heavy chain V region - mouse >g...	387	5.7e-58	2
pir S25175 S25175	Ig heavy chain V region - mouse >g...	399	5.8e-58	2
pir A24672 A24672	Ig heavy chain precursor V region ...	395	5.8e-58	2
gp M60237 MUSIGHP111_1	immunoglobulin heavy chain [Mus mu...	455	5.9e-58	1
gp X82581 MMIGPE2_1	IgG heavy chain [Mus musculus]	389	6.0e-58	2
gp U07214 MMU07214_1	anti-C5a Ig heavy chain V region [...	455	6.1e-58	1
gp M64134 MUSIGHNOE_1	Ig heavy chain [Mus musculus]	395	6.1e-58	2
gp M64142 MUSIGHNOM_1	Ig heavy chain [Mus musculus]	395	6.2e-58	2
gp S71019 S71019_1	anti-erbB-2 product monoclonal ant...	394	6.4e-58	2
sp P01751 HV07_MOUSE	IG HEAVY CHAIN PRECURSOR V REGION ...	394	6.8e-58	2
gp U26992 MMU26992_1	Ig variable region [Mus musculus]	382	6.9e-58	2
gp M28529 MUSIGHMO_1	Mouse active Ig mu-chain VJ3-regio...	282	7.8e-58	3
pir A22769 A22769	Ig heavy chain V region (B1-8) - m...	394	7.9e-58	2
gp M26808 MUSIGHADM_1	Mouse Ig heavy chain mRNA V-region...	394	7.9e-58	2
gp Z22024 MDIGMVAA_1	immunoglobulin variable region [Mu...	403	8.3e-58	2

WARNING: Descriptions of 8535 database sequences were not reported due to the limiting value of parameter V = 100.

>gp|x64805|MMAIDHCH_1 anti-Id mAb 114 haevy chain, V-region [Mus musculus]
Length = 118

Score = 542 (246.4 bits), Expect = 7.4e-70, P = 7.4e-70
Identities = 100/118 (84%), Positives = 110/118 (93%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPQGGLWIGNIFPGNGDTYY 60
QAYLQQSGAELVR G+SVKMSCKASGYT TSYNMHVVKQTP QGLEWIG I+PGNGDT Y
Sbjct: 1 QAYLQQSGAELVRPGSSVKMSCKASGYTFTSYNMHVVKQTPRQGLEWIGAIYPGNGDTSY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYWGQGTSTVSS 118
NQKFKGKA+LT D SSSTAYMQ+SSLTSEDSAVYFCARG++ G++DYWGQGT++TVSS
Sbjct: 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARGDYSIDYWGQGTTLTVSS 118

>gp|m17953|MUSIGHXW_1 immunoglobulin heavy chain [Mus musculus]
Length = 140

Score = 462 (210.0 bits), Expect = 4.2e-65, Sum P(2) = 4.2e-65
Identities = 88/98 (89%), Positives = 91/98 (92%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGGGLEWIGNIFPGNGDTYY 60
QAYLQQSGAELVR GASVKMSCKASGYT TSYNMHWVKQTP QGLEWIG I+PGNGDT Y
Sbjct: 20 QAYLQQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPNGDTSY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCAR 98
NQKFKGKA+LT D SSSTAYMQ+SSLTSSEDSAVYFCAR
Sbjct: 80 NQKFKGKATLTVDKSSSTAYMQLSSLTSSEDSAVYFCAR 117

Score = 50 (22.7 bits), Expect = 4.2e-65, Sum P(2) = 4.2e-65
Identities = 9/12 (75%), Positives = 10/12 (83%)

Query: 106 DYWGQGTSTVVS 117
D WG GT+VTVS
Sbjct: 129 DVWGTTTSTVVS 140

>gp|Z22117|MDIGGVBC_1 immunoglobulin variable region [Mus musculus domesticus]
Length = 120

Score = 430 (195.5 bits), Expect = 2.3e-64, Sum P(2) = 2.3e-64
Identities = 80/98 (81%), Positives = 88/98 (89%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGGGLEWIGNIFPGNGDTYY 60
+ LQQSG ELV+ GASVK+SCKASGYT T Y MHWVKQ PGQGLEWIG I+PG+G+TTY
Sbjct: 1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYMHVWVKQKPGQGLEWIGEIYPGSGNTYY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCAR 98
N+KFKGKASLTAD SSSTAYMQ+SSLTSSEDSAVYFCAR
Sbjct: 61 NEKFKGKASLTADKSSSTAYMQLSSLTSSEDSAVYFCAR 98

Score = 77 (35.0 bits), Expect = 2.3e-64, Sum P(2) = 2.3e-64
Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVSS 118
A+DYWGQGTSTVSS
Sbjct: 106 AMDYWGGTSTVSS 120

>gp|U10410|MMU10410_1 antineuraminidase single chain antibody [Mus musculus]
Length = 273

Score = 425 (193.2 bits), Expect = 1.3e-63, Sum P(2) = 1.3e-63
Identities = 79/98 (80%), Positives = 89/98 (90%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGGGLEWIGNIFPGNGDTYY 60
Q LQQSGAELV+ GASV+MSCKASGYT T+YNM+VVKQ+PGQGLEWIG +PGNGDT Y
Sbjct: 23 QVQLQQSGAELVKPGASVMSCKASGYTFTNYMYVVKQSPGGGLEWIGIFYPNGDTSY 82

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCAR 98
NQKFK KA+LTAD SS+TAYMQ+SSLTSSEDSAVY+CAR
Sbjct: 83 NQKFKDKATLTADKSSNTAYMQLSSLTSSEDSAVYFCAR 120

Score = 74 (33.6 bits), Expect = 1.3e-63, Sum P(2) = 1.3e-63
Identities = 12/17 (70%), Positives = 15/17 (88%)

Query: 101 WEGALDYWGQGTSTVVS 117
++G DYWGQGT+VTVS
Sbjct: 127 YDGGFDYWGGTTTSTVVS 143

>pir|S38950|S38950 Ig gamma chain - mouse
Length = 246

Score = 420 (190.9 bits), Expect = 2.6e-63, Sum P(2) = 2.6e-63
Identities = 79/99 (79%), Positives = 88/99 (88%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQSG ELVR GASVK+SCKASGYT T Y +HWVKQ PG+GLEWIG I+PG+G+T Y
 Sbjct: 1 QIQLQQSGPELVKPGASVKISCKASGYTFTDYYIHVVKQRPGEGLWIGWIYPGSGNTKY 60

Query: 61 NQKFKGKASLTADTSSTAYMQISLTSEDSAVYFCARG 99
 N+KFKGKA+LT DTSSSTAYMQ+SSLTSEDSAVYFCARG
 Sbjct: 61 NEKFKGKATLTVDTSSTAYMQLSSLTSEDSAVYFCARG 99

Score = 77 (35.0 bits), Expect = 2.6e-63, Sum P(2) = 2.6e-63
 Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTVSS 118
 A+DYWGQGTSTVTVSS
 Sbjct: 103 AMDYWGQGTSTVTVSS 117

>gp|Z22034|MDIGGVAG_1 immunoglobulin variable region [Mus musculus domesticus]
 Length = 119

Score = 421 (191.4 bits), Expect = 4.0e-63, Sum P(2) = 4.0e-63
 Identities = 79/104 (75%), Positives = 90/104 (86%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQSG ELV+ GASVK+SCKASGYT T Y +HWVKQ+PGQGLEWIG I+PG+G+T Y
 Sbjct: 1 QVQLQQSGPELVKPGASVKLSCKASGYTFTDYYIHVVKQSPGQGLEWIGWIYPGSGNTKY 60

Query: 61 NQKFKGKASLTADTSSTAYMQISLTSEDSAVYFCARGNWEA 104
 N KFKGKA++TAD SSSTAYMQ+SSLTSEDSAVYFCARG G+
 Sbjct: 61 NDKFKGKATMTADKSSSTAYMQLSSLTSEDSAVYFCARGVARG 104

Score = 77 (35.0 bits), Expect = 4.0e-63, Sum P(2) = 4.0e-63
 Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTVSS 118
 A+DYWGQGTSTVTVSS
 Sbjct: 105 AMDYWGQGTSTVTVSS 119

>gp|U40581|MMU40581_1 sFv antibody [Mus musculus]
 Length = 246

Score = 409 (185.9 bits), Expect = 1.1e-61, Sum P(2) = 1.1e-61
 Identities = 78/99 (78%), Positives = 85/99 (85%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQ+SGAELV+ GASVK+SCKASGYT TSY MHWVKQ PGQGLEWIG I P NG T Y
 Sbjct: 1 QVQLQESGAELVKPGASVKLSCKASGYTFTSYMHWVKQRPQGLEWIGKINPSNGRTNY 60

Query: 61 NQKFKGKASLTADTSSTAYMQISLTSEDSAVYFCARG 99
 N+KFK KA+LT D SSSTAYMQ+SSLTSEDSAVY+CARG
 Sbjct: 61 NEKFKKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARG 99

Score = 76 (34.5 bits), Expect = 1.1e-61, Sum P(2) = 1.1e-61
 Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTVSS 118
 ALDYWGQGT+VTVSS
 Sbjct: 109 ALDYWGQGT+VTVSS 123

Score = 50 (22.7 bits), Expect = 0.0083, Sum P(3) = 0.0083
 Identities = 8/20 (40%), Positives = 14/20 (70%)

Query: 81 MQISLTSEDSAVYFCARGN 100
 + I+S+ +ED +YFC + N
 Sbjct: 211 LSINSVETEDFGMYFCQQSN 230

Score = 39 (17.7 bits), Expect = 0.0083, Sum P(3) = 0.0083
 Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 12 VRSGASVKMSCKAS 25
V G SV +SC+AS
Sbjct: 151 VTPGDSVSLSCRAS 164

Score = 34 (15.5 bits), Expect = 0.0083, Sum P(3) = 0.0083
Identities = 5/9 (55%), Positives = 7/9 (77%)

Query: 31 SYNMHVVKQ 39
S N+HW +Q
Sbjct: 168 SNNLHWYQQ 176

>gp|A13735|A13735_1 V region monoclonal antibody, cross reacts with 19 known
P.aeruginosa serotypes [unidentified] >gp|M28834|MUSIGHALPA_1
immunoglobulin gamma-2a chain [Mus musculus]
Length = 159

Score = 390 (177.3 bits), Expect = 1.3e-61, Sum P(2) = 1.3e-61
Identities = 76/98 (77%), Positives = 81/98 (82%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYY 60
Q LQQSGAEL + GASVKMSCKASGYT T+Y MHVVKQ PGQGLEWIG I P G T Y
Sbjct: 20 QVQLQQSGAELAKPGASVKMSCKASGYTFTAYWMHVVKQRPQGLEWIGYINPNTGYTEY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCAR 98
NQ FK KA+LTAD SSSTAYMQ+SSLTSEDSAVY+C R
Sbjct: 80 NQNFKDKATLTADKSSSTAYMQLSSLTSEDSAVYYCTR 117

Score = 96 (43.6 bits), Expect = 1.3e-61, Sum P(2) = 1.3e-61
Identities = 17/19 (89%), Positives = 19/19 (100%)

Query: 100 NWEALDYWGQGSTVTVSS 118
N+EGA+DYWGQGSTVTVSS
Sbjct: 121 NYEGAMDYWGQGSTVTVSS 139

>pir|PS0024|PS0024 Ig heavy chain precursor V region (6A4) - mouse
Length = 139

Score = 390 (177.3 bits), Expect = 1.5e-61, Sum P(2) = 1.5e-61
Identities = 76/98 (77%), Positives = 81/98 (82%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYY 60
Q LQQSGAEL + GASVKMSCKASGYT T+Y MHVVKQ PGQGLEWIG I P G T Y
Sbjct: 20 QVQLQQSGAELAKPGASVKMSCKASGYTFTAYWMHVVKQRPQGLEWIGYINPNTGYTEY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCAR 98
NQ FK KA+LTAD SSSTAYMQ+SSLTSEDSAVY+C R
Sbjct: 80 NQNFKDKATLTADKSSSTAYMQLSSLTSEDSAVYYCTR 117

Score = 96 (43.6 bits), Expect = 1.5e-61, Sum P(2) = 1.5e-61
Identities = 17/19 (89%), Positives = 19/19 (100%)

Query: 100 NWEALDYWGQGSTVTVSS 118
N+EGA+DYWGQGSTVTVSS
Sbjct: 121 NYEGAMDYWGQGSTVTVSS 139

>gp|222059|MDIGGVAN_1 immunoglobulin variable region [Mus musculus domesticus]
Length = 121

Score = 417 (189.6 bits), Expect = 1.7e-61, Sum P(2) = 1.7e-61
Identities = 79/100 (79%), Positives = 89/100 (89%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYY 60
Q LQQSG ELVR GASVK+SCKASGYT T Y ++VVKQ PGQGLEWIG I+PG+G+T Y
Sbjct: 1 QIQLQQSGPELVRPGASVKISCKASGYTFTDYYINWVKQRPQGLEWIGWIYPGSGNTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCARGN 100

N+KFKGKA+LT DTSSSTAYMQ+SSLTSEDSAVYFCARG+
 Sbjct: 61 NEKFKGKATLTVDTSSTAYMQLSSLTSEDSAVYFCARGD 100

Score = 69 (31.4 bits), Expect = 1.7e-61, Sum P(2) = 1.7e-61
 Identities = 12/14 (85%), Positives = 14/14 (100%)

Query: 105 LDYWGQGTSTVSS 118
 LDYWGQGT++TVSS
 Sbjct: 108 LDYWGQGTTLTVSS 121

>pir|E48677|E48677 Ig heavy chain V-D-J region (48) - mouse (fragment)
 Length = 123

Score = 404 (183.7 bits), Expect = 3.1e-61, Sum P(2) = 3.1e-61
 Identities = 78/108 (72%), Positives = 89/108 (82%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQSGAELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG Y
 Sbjct: 1 QVRLQQSGAELVRAGSSVKMSCKASGYTFTSYGVNVVKQRPQGLEWIGYINPGNGYINY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYW 108
 N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAV+FCAR ++ G Y+
 Sbjct: 61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVFFCARSSYFGGGYYY 108

Score = 80 (36.4 bits), Expect = 3.1e-61, Sum P(2) = 3.1e-61
 Identities = 15/20 (75%), Positives = 17/20 (85%)

Query: 99 GNWEALDYWGQGTSTVSS 118
 G + A+DYWGQGTSTVSS
 Sbjct: 104 GGGYYAMDYWGQGTSTVSS 123

>gp|M32037|MUSIGHRK_1 Mouse Ig H-chain mRNA V-D-J region, from hybridoma
 P6514-2, partial cds. [Mus musculus] >gp|M32038|MUSIGHRL_1 Mouse Ig
 H-chain mRNA V-D-J region, from hybridoma P65J4-1, partial cds.
 [Mus musculus]
 Length = 121

Score = 419 (190.5 bits), Expect = 3.1e-61, Sum P(2) = 3.1e-61
 Identities = 80/108 (74%), Positives = 90/108 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSGAELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG T Y
 Sbjct: 1 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINVVKQRPQGLEWIGYINPGNGYTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYW 108
 N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR N+ G Y+
 Sbjct: 61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSNYGGSYFF 108

Score = 65 (29.5 bits), Expect = 3.1e-61, Sum P(2) = 3.1e-61
 Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVSS 118
 DYWGQGT++TVSS
 Sbjct: 109 DYWGQGTTLTVSS 121

>pir|S41394|S41394 Ig heavy chain V region - mouse
 Length = 120

Score = 407 (185.0 bits), Expect = 8.1e-61, Sum P(2) = 8.1e-61
 Identities = 78/98 (79%), Positives = 84/98 (85%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSGAELV+ GASVK+SCKASGYT TSY MHVVKQ PGQGLEWIG I P + TYY
 Sbjct: 1 EVQLQQSGAELVKPGASVKLSCKASGYTFTSYMHVVKQRPQGLEWIGEIDPSDSYTTY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR 98

NQKFKGKA+LT D SSSTAYMQ SSLTSEDSAVY+CAR
 Sbjct: 61 NQKFKGKATLTVDKSSSTAYMQSSLTSEDSAVYYCAR 98

Score = 74 (33.6 bits), Expect = 8.1e-61, Sum P(2) = 8.1e-61
 Identities = 13/15 (86%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTSS 118
 ++DYWGQGTSTVTSS
 Sbjct: 106 SMDYWGQGTSTVTSS 120

>gp|S69279|S69279_1 anti-louping ill virus antibody 4.2 heavy-chain variable
 region [Mus sp.]
 Length = 120

Score = 405 (184.1 bits), Expect = 8.1e-61, Sum P(2) = 8.1e-61
 Identities = 77/99 (77%), Positives = 85/99 (85%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQSG ELV+ GASVKMSCKASGYT T Y + WVKQ GQGLEWIG I+PG+G TYY
 Sbjct: 1 QVQLQQSGPELVKPGASVKMSCKASGYTFDVIWVVKQRTGQGLEWIGEIYPGSGTYY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG 99
 N+KFK KA+LTAD SS+TAYMQ+SSLTSEDSAVYFCARG
 Sbjct: 61 NEKFKDKATLTADKSSNTAYMQLSSLTSEDSAVYFCARG 99

Score = 76 (34.5 bits), Expect = 8.1e-61, Sum P(2) = 8.1e-61
 Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTSS 118
 ALDYWGQGT+VTSS
 Sbjct: 106 ALDYWGQGT+VTSS 120

>gp|Z22088|MDIGGVAR_1 immunoglobulin variable region [Mus musculus domesticus]
 Length = 119

Score = 407 (185.0 bits), Expect = 8.1e-61, Sum P(2) = 8.1e-61
 Identities = 78/103 (75%), Positives = 84/103 (81%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQS AEL R GASVKMSCKASGYT T Y MHWVKQ PGQ LEWIG I+PGN DT Y
 Sbjct: 1 QVQLQQSEAEARPGASVKMSCKASGYTFTRYMMHWVKQRPQGLEWIGAIYPGNSDTNY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWE 103
 NQKFKGKA LTA TS+STAYM++SSL SEDSAVY+CAR + G
 Sbjct: 61 NQKFKGKALTA VTSASTAYMELSSLASEDSAVYFCARSRYG 103

Score = 74 (33.6 bits), Expect = 8.1e-61, Sum P(2) = 8.1e-61
 Identities = 13/15 (86%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTSS 118
 ++DYWGQGTSTVTSS
 Sbjct: 105 SMDYWGQGTSTVTSS 119

>pir|F48677|F48677 Ig heavy chain V-D-J region (44.1) - mouse (fragment)
 Length = 123

Score = 400 (181.8 bits), Expect = 1.1e-60, Sum P(2) = 1.1e-60
 Identities = 77/108 (71%), Positives = 89/108 (82%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQSGAELVR+G+SVK+SCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG Y
 Sbjct: 1 QVRLQQSGAELVRAGSSVKISCKASGYTFTSYGVNHWVKQRPQGLEWIGYINPGNGYIKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYW 108
 N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAV+FCAR ++ G Y+
 Sbjct: 61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVFFCARSSYFGGGYY 108

Score = 80 (36.4 bits), Expect = 1.1e-60, Sum P(2) = 1.1e-60
Identities = 15/20 (75%), Positives = 17/20 (85%)

Query: 99 GNWEGALDYWGQGSTVTVSS 118
G + A+DYWGQGSTVTVSS
Sbjct: 104 GGYYYAMDYWGQGSTVTVSS 123

>gp|L22747|MUSF_1 immunoglobulin heavy chain [Mus musculus]
Length = 118

Score = 475 (215.9 bits), Expect = 1.1e-60, P = 1.1e-60
Identities = 90/118 (76%), Positives = 103/118 (87%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVWKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQSGAELVR G SVK+SCKASGYT T+Y + WVKQ PG GLEWIG+I+PG G T Y
Sbjct: 1 QVQLQQSGAELVRPGTSVKISCKASGYTFTNYWLGWVKQRPQGHGLEWIGDIYPGGGYTNY 60
Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYWGQGSTVTVSS 118
N+KFKGKA+LTADTSSSTAYMQ+SSLTSEDSAVYFCAR ++ G+ DYWGQGT++TVSS
Sbjct: 61 NEKFKGKATLTADTSSSTAYMQLSLTSEDSAVYFCARPHYYGSGDYWGQGTTLTVSS 118

>gp|M32036|MUSIGHRJ_1 Mouse Ig H-chain mRNA V-D-J region, from hybridoma
P65D6-3, partial cds. [Mus musculus]
Length = 121

Score = 414 (188.2 bits), Expect = 1.5e-60, Sum P(2) = 1.5e-60
Identities = 79/108 (73%), Positives = 90/108 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVWKQTPGQGLEWIGNIFPGNGDTYY 60
+ LQQSGAELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG T Y
Sbjct: 1 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPQGLEWIGYINPGNGYTKY 60
Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYW 108
N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR ++ G Y+
Sbjct: 61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYYGGSYYF 108

Score = 65 (29.5 bits), Expect = 1.5e-60, Sum P(2) = 1.5e-60
Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGSTVTVSS 118
DYWGQGT++TVSS
Sbjct: 109 DYWGQGTTLTVSS 121

>pir|A26405|A26405 Ig heavy chain V region (3D10) - mouse
Length = 121

Score = 400 (181.8 bits), Expect = 1.5e-60, Sum P(2) = 1.5e-60
Identities = 75/103 (72%), Positives = 86/103 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVWKQTPGQGLEWIGNIFPGNGDTYY 60
+ LQQSG ELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG T Y
Sbjct: 1 EVQLQQSGTELVRAGSSVKMSCKASGYTFTSYGINWVKQRPQGLEWIGYINPGNGYTKY 60
Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWE 103
N+KFKGK +LT D SSSTAYMQ+ SLTSED+AVYFC+R + G
Sbjct: 61 NEKFKGKTTLTVDRSSSTAYMQLRSLTSEDAAVYFCRSEYYG 103

Score = 79 (35.9 bits), Expect = 1.5e-60, Sum P(2) = 1.5e-60
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGSTVTVSS 118
ALDYWGQGSTVTVSS
Sbjct: 107 ALDYWGQGSTVTVSS 121

>gp|U26991|MMU26991_1 Ig variable region [Mus musculus]
Length = 137

Score = 473 (215.0 bits), Expect = 1.8e-60, P = 1.8e-60
Identities = 90/118 (76%), Positives = 99/118 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
+ LQQSG ELV+ GASVKMSCKASGYT TSY MHWVKQ PGQGLEWIG I P N T Y
Sbjct: 20 EVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTKY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTVTVSS 118
N+KFKGKA+LT+D SSSTAYM++SSLTSEDSAVY+CAR W +DYWGQGTSTVTVSS
Sbjct: 80 NEKFKGKATLTSKSSSTAYMELSSLTSEDSAVYYCARNGLPPMDYWGQGTSTVTVSS 137

>pir|PL0208|PL0208 anti-idiotypic antibody E225, gamma chain V region - mouse
(strain BALB/c) (fragment)
Length = 136

Score = 418 (190.0 bits), Expect = 1.8e-60, Sum P(2) = 1.8e-60
Identities = 77/99 (77%), Positives = 88/99 (88%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQ G+ELVR GASVK+SCKASGYT T+Y MHWVKQ PGQGLEWIGNI+PG+GD+ Y
Sbjct: 20 QVQLQQPGSELVRPGASVKLSCKASGYTFTNYMHWVKQRPQGLEWIGNIYPGSGDSNY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARG 99
++KFK KA+LT DTSSSTAYMQ+S LTSEDSAVY+CARG
Sbjct: 80 DEKFKSKATLTVDTSSTAYMQLSGLTSEDSAVYYCARG 118

Score = 60 (27.3 bits), Expect = 1.8e-60, Sum P(2) = 1.8e-60
Identities = 10/13 (76%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTVSS 118
D+WGQGT++TVSS
Sbjct: 124 DHWGQGTTLTVSS 136

>gp|X53637|MME225H_1 E225 gene product [Mus musculus]
Length = 136

Score = 418 (190.0 bits), Expect = 1.8e-60, Sum P(2) = 1.8e-60
Identities = 77/99 (77%), Positives = 88/99 (88%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQ G+ELVR GASVK+SCKASGYT T+Y MHWVKQ PGQGLEWIGNI+PG+GD+ Y
Sbjct: 20 QVQLQQPGSELVRPGASVKLSCKASGYTFTTYMHWVKQRPQGLEWIGNIYPGSGDSNY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARG 99
++KFK KA+LT DTSSSTAYMQ+S LTSEDSAVY+CARG
Sbjct: 80 DEKFKSKATLTVDTSSTAYMQLSGLTSEDSAVYYCARG 118

Score = 60 (27.3 bits), Expect = 1.8e-60, Sum P(2) = 1.8e-60
Identities = 10/13 (76%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTVSS 118
D+WGQGT++TVSS
Sbjct: 124 DHWGQGTTLTVSS 136

>gp|M34581|MUSIGHABU_1 Mouse Ig heavy-chain mRNA V-D-J region, partial cds.
[Mus musculus] >gp|M31956|MUSIGHRO_1 Mouse Ig active mu-chain mRNA
V-D-J2 region, from hybridoma CH12, partial cds. [Mus musculus]
Length = 122

Score = 408 (185.5 bits), Expect = 2.0e-60, Sum P(2) = 2.0e-60
Identities = 78/108 (72%), Positives = 87/108 (80%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60

11D10 Heavy Chain PEPTIDE – 12

Q LQQ G ELV+ GASVK+SCKASGYT TSY MHVVKQ PGQGLEWIGNI P NG T Y
Sbjct: 1 QVQLQQPGTGLVKPGASVKLSCKASGYTFTSYMHVVKQRPQGQLEWIGNINPSNGGTNY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEGALDYW 108

N+KFK KA+LT D SSSTAYMQ+SSLTSEDSAVY+CAR + + Y+
Sbjct: 61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYVCARDYYGSSWGY 108

Score = 70 (31.8 bits), Expect = 2.0e-60, Sum P(2) = 2.0e-60
Identities = 12/19 (63%), Positives = 15/19 (78%)

Query: 100 NWEALDYWGQGTSTVTVSS 118

+W DYWGQGT++TVSS
Sbjct: 104 SWGYFDYWGQGTTLTVSS 122

>gp|L24557|MUSIGHMADQ_1 immunoglobulin heavy chain [Mus musculus]
Length = 122

Score = 401 (182.3 bits), Expect = 2.0e-60, Sum P(2) = 2.0e-60
Identities = 76/98 (77%), Positives = 85/98 (86%)

Query: 4 LQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPQGQLEWIGNIFPGNGDTYYNQK 63

LQ+SGAEL R GASVKMSCKASGYT + Y+MHVVKQ PGQGLEWIG I+P +G T YNQK
Sbjct: 3 LQESGAELARPGASVKMSCKASGYTFSRYSMHVVKQRPQGQLEWIGIYPTSGYTNYNQK 62

Query: 64 FKKGASLTADTSSSTAYMQISLTSSEDSAVYFCARGNW 101

FK KA+LTAD SSSTAYMQ+SSLTSEDSAVY+CAR +
Sbjct: 63 FKDKATLTADKSSSTAYMQLSSLTSEDSAVYVCARSEY 100

Score = 77 (35.0 bits), Expect = 2.0e-60, Sum P(2) = 2.0e-60
Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTVSS 118

A+DYWGQGTSTVTVSS
Sbjct: 108 AMDYWGQGTSTVTVSS 122

>gp|M36210|MUSIGHADQ_1 immunoglobulin heavy chain V-region [Mus musculus]
Length = 119

Score = 422 (191.8 bits), Expect = 2.1e-60, Sum P(2) = 2.1e-60
Identities = 80/101 (79%), Positives = 89/101 (88%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPQGQLEWIGNIFPGNGDTYY 60

Q LQQSGAELVR G SVK+SCKASGYT T+Y + VVKQ PG GLEWIG+I+PG G T Y
Sbjct: 1 QVQLQQSGAELVRPGTSVKISCKASGYTFTNYWLVGQRPQGHLEWIGDIYPGGYTY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNW 101

N+KFKGKA+LTADTSSSTAYMQ+SSLTSEDSAVYFCARGN+
Sbjct: 61 NEKFKGKATLTADTSSSTAYMQLSSLTSEDSAVYFCARGNY 101

Score = 56 (25.5 bits), Expect = 2.1e-60, Sum P(2) = 2.1e-60
Identities = 10/12 (83%), Positives = 11/12 (91%)

Query: 107 YWGQGTSTVTVSS 118

YWGQGT VTVS+
Sbjct: 108 YWGQGTTLTVSA 119

>gp|M28251|MUSIGHMX_1 Mouse Ig rearranged gamma-chain (G-2a) mRNA V-region
(V-J2), partial cds. [Mus musculus]
Length = 136

Score = 406 (184.6 bits), Expect = 2.5e-60, Sum P(2) = 2.5e-60
Identities = 79/99 (79%), Positives = 83/99 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPQGQLEWIGNIFPGNGDTYY 60

Q LQQSGAEL + GASVKMSCKASGYT TSY MHVVKQ PGQGLEWIG I P G T Y
Sbjct: 20 QVQLQQSGAELAKPGASVKMSCKASGYTFTSYRMHVVKQRPQGQLEWIGIYINPSTGYTEY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARG 99
 NQKFK KA+LTAD SSSTAYMQ+SSLT EDSAVY+CARG
 Sbjct: 80 NQKFKDKATLTADKSSSTAYMQLSSLTFEDSAVYYCARG 118

Score = 71 (32.3 bits), Expect = 2.5e-60, Sum P(2) = 2.5e-60
 Identities = 12/16 (75%), Positives = 14/16 (87%)

Query: 103 GALDYWGQGTSTVTVSS 118
 G DYWGQGT++TVSS
 Sbjct: 120 GVFDYWGQGTTLTVSS 135

>gp|Z22129|MDIGMVC_1 immunoglobulin variable region [Mus musculus domesticus]
 Length = 121

Score = 400 (181.8 bits), Expect = 2.8e-60, Sum P(2) = 2.8e-60
 Identities = 77/104 (74%), Positives = 87/104 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSG ELV+ GASVKMSCKASGYT TSY MHVVKQ PGQGLEWIG I P N T Y
 Sbjct: 1 EVLQQSGPELVKPGASVKMSCKASGYTFTSYVMHVVKQKPGQGLEWIGYINPYNDGTY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEA 104
 N+KFKGKA+LT+D SSSTAYM++SSLTSSEDSAVY+CAR + G+
 Sbjct: 61 NEKFKGKATLTSDKSSSTAYMELSSLTSSEDSAVYYCARRGYYS 104

Score = 77 (35.0 bits), Expect = 2.8e-60, Sum P(2) = 2.8e-60
 Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTVSS 118
 A+DYWGQGTSTVTVSS
 Sbjct: 107 AMDYWGQGTSTVTVSS 121

>pir|S26309|S26309 Ig heavy chain V region - mouse
 Length = 116

Score = 394 (179.1 bits), Expect = 2.9e-60, Sum P(2) = 2.9e-60
 Identities = 74/99 (74%), Positives = 84/99 (84%)

Query: 5 QQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYYNQKF 64
 QQSG+ELVR GASVK+SCKASGYT TSY MHVVKQ GQGLEWIGNI+PG+G T Y++KF
 Sbjct: 1 QQSGSELVRPGASVKLSCKASGYTFTSYMHVVKQRHGQGLEWIGNIYPGSGSTNYDEKF 60

Query: 65 KGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWE 103
 K K +LT DTSSSTAYM +SSLTSSEDSAVY+C R +G
 Sbjct: 61 KSKGTLTVDTSSTAYMHLSSLTSSEDSAVYYCTREDDG 99

Score = 83 (37.7 bits), Expect = 2.9e-60, Sum P(2) = 2.9e-60
 Identities = 15/16 (93%), Positives = 16/16 (100%)

Query: 103 GALDYWGQGTSTVTVSS 118
 GA+DYWGQGTSTVTVSS
 Sbjct: 101 GAMDYWGQGTSTVTVSS 116

>gp|M32035|MUSIGHRI_1 Mouse Ig H-chain mRNA V-D-J region, from hybridoma
 P65D6-7, partial cds. [Mus musculus]
 Length = 121

Score = 411 (186.8 bits), Expect = 3.8e-60, Sum P(2) = 3.8e-60
 Identities = 78/103 (75%), Positives = 88/103 (85%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSGAELVR+G+SVKMSCKASGYT TSY ++VVKQ PGQGLEWIG I PGNG T Y
 Sbjct: 1 EVLQQSGAELVRAGSSVKMSCKASGYTFTSYGINVVKQRPQGLEWIGYINPGNGYTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWE 103

N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR ++ G
 Sbjct: 61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYYG 103

Score = 65 (29.5 bits), Expect = 3.8e-60, Sum P(2) = 3.8e-60
 Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTSS 118

DYWGQGT++TVSS

Sbjct: 109 DYWGQGTTLTVSS 121

>gp|S74051|S74051_1 Ig VH gene product [Mus sp.]
 Length = 114

Score = 471 (214.1 bits), Expect = 4.0e-60, P = 4.0e-60
 Identities = 86/114 (75%), Positives = 99/114 (86%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSG ELV+ GASVK+SCKASGYT T Y MHWV+Q PGQGLEWIG I+PG+G+T Y

Sbjct: 1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYMMHWVRQRPQGQGLEWIGIYPGSGNTSY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYWGQGTSV 114

N+KF+GKA+LTAD SSSTAYMQ+SSLTSEDSAVYFCARG + +DYWGQGTSV

Sbjct: 61 NEKFRGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARGTLDYTM DYWGQGTSV 114

>pir|PH1482|PH1482 Ig heavy chain V region (clones 36-35[IG] and X7-TG) - mouse
 (fragment)
 Length = 140

Score = 410 (186.4 bits), Expect = 4.5e-60, Sum P(2) = 4.5e-60
 Identities = 79/108 (73%), Positives = 89/108 (82%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSGAELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG T Y

Sbjct: 20 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPQGQGLEWIGYINPGNGYTKY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYW 108

N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR + G Y+

Sbjct: 80 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYGGSYFF 127

Score = 65 (29.5 bits), Expect = 4.5e-60, Sum P(2) = 4.5e-60
 Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTSS 118

DYWGQGT++TVSS

Sbjct: 128 DYWGQGTTLTVSS 140

>gp|x06110|MMIGVHD1_1 Mouse mRNA (36-35) for immunoglobulin heavy chain
 VDJ-region. [Mus musculus] >gp|M20274|MUSIGHKA_1 Mouse Ig active
 gamma chain mRNA V-region VDJH2, partial cds, clone 36-65. [Mus
 musculus] >gp|M20275|MUSIGHKB_1 Mouse Ig active gamma chain mRNA
 V-region VDJH2, partial cds, clone 4F8. [Mus musculus]
 >gp|M20276|MUSIGHKC_1 Mouse Ig active gamma chain mRNA V-region
 VDJH2, partial cds, clone 26C2. [Mus musculus]
 >gp|M20277|MUSIGHKD_1 Mouse Ig active gamma chain mRNA V-region
 VDJH2, partial cds, clone 24F3. [Mus musculus]
 >gp|M19292|MUSIGHXK_1 Mouse IgG active H-chain gene VDJ2-region
 from hybridoma cell-line 36-65. [Mus musculus]
 Length = 121

Score = 410 (186.4 bits), Expect = 5.2e-60, Sum P(2) = 5.2e-60
 Identities = 79/108 (73%), Positives = 89/108 (82%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTPGQGLEWIGNIFPGNGDTYY 60

+ LQQSGAELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG T Y

Sbjct: 1 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPQGQGLEWIGYINPGNGYTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYW 108
 N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR + G Y+
 Sbjct: 61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYGGSYF 108

Score = 65 (29.5 bits), Expect = 5.2e-60, Sum P(2) = 5.2e-60
 Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTSS 118
 DYWGQGT++TVSS
 Sbjct: 109 DYWGQGTTLTVSS 121

>gp|222134|MDIGMVB1 immunoglobulin variable region [Mus musculus domesticus]
 Length = 121

Score = 401 (182.3 bits), Expect = 5.2e-60, Sum P(2) = 5.2e-60
 Identities = 77/99 (77%), Positives = 85/99 (85%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYMMHWKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSG ELV+ GASVKMSCKASGYT TSY MHWVKQ PGQGLEWIG I P N T Y
 Sbjct: 1 EVLQQSGPELVKPGASVKMSCKASGYTFTSYMMHWKQKPGQGLEWIGYINPYNDGTY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG 99
 N+KFKGKA+LT+D SSSTAYM++SSLTSEDSAVY+CARG
 Sbjct: 61 NEKFKGKATLTSKSSSTAYMELSSLTSEDSAVYFCARG 99

Score = 74 (33.6 bits), Expect = 5.2e-60, Sum P(2) = 5.2e-60
 Identities = 13/15 (86%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTSS 118
 A+DYWG+GTSVTSS
 Sbjct: 107 AMDYWGEGTSTVTSS 121

>gp|K00684|MUSIGHBG1 Mouse Ig active H-chain V-region from B1-8.V1, subgroup
 VH-II. [Mus musculus]
 Length = 139

Score = 409 (185.9 bits), Expect = 6.2e-60, Sum P(2) = 6.2e-60
 Identities = 80/117 (68%), Positives = 92/117 (78%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYMMHWKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQ GAELV+ GASVK+SCKASGYT TSY MHWVKQ PGQGLEWIG I P + DT Y
 Sbjct: 20 QVQLQPGAEVLKPGASVKVCKASGYTFTSYMMHWKQRPQGLEWIGRIHPSDSDTNY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYWGQGTSTVTS 117
 NQKFKGKA+LT D SSTAYMQ+SSLTSEDSAVY+CAR ++ G+ + G T++
 Sbjct: 80 NQKFKGKATLTDKPSSTAYMQLSSLTSEDSAVYFCARYDYGGSYFDYWGQGTTLT 136

Score = 65 (29.5 bits), Expect = 6.2e-60, Sum P(2) = 6.2e-60
 Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTSS 118
 DYWGQGT++TVSS
 Sbjct: 127 DYWGQGTTLTVSS 139

>sp|P01747|HV03_MOUSE IG HEAVY CHAIN V REGION (36-65).
 Length = 120

Score = 409 (185.9 bits), Expect = 7.2e-60, Sum P(2) = 7.2e-60
 Identities = 79/105 (75%), Positives = 88/105 (83%)

Query: 4 LQQSGAELVRSGASVKMSCKASGYTLTSYMMHWKQTPGQGLEWIGNIFPGNGDTYYNQK 63
 LQQSGAELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG T YN+K
 Sbjct: 3 LQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPQGLEWIGYINPGNGYTYNEK 62

Query: 64 FKFKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYW 108
 FKFK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR + G Y+

Sbjct: 63 FKGKTTTLVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYGGSYYF 107

Score = 65 (29.5 bits), Expect = 7.2e-60, Sum P(2) = 7.2e-60
Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTSS 118
DYWGQGT++TVSS

Sbjct: 108 DYWGQGTTLTVSS 120

>pir|B22769|B22769 Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative
sequence)
Length = 120

Score = 409 (185.9 bits), Expect = 7.2e-60, Sum P(2) = 7.2e-60
Identities = 80/117 (68%), Positives = 92/117 (78%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQ GAELV+ GASVK+SCKASGYT TSY MHVVKQ PGQGLEWIG I P + DT Y

Sbjct: 1 QVQLQQPGAELVKPGASVKVCKASGYTFTSYMHVVKQRPQGQGLEWIGRIHPSDSDTNY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTVTS 117
NQKFKGKA+LT D SSTAYMQ+SSLTSEDSAVY+CAR ++ G+ + G T++

Sbjct: 61 NQKFKGKATLTVDKPSSTAYMQLSSLTSEDSAVYFCARYDYWGSSYFDYWGQGTTLT 117

Score = 65 (29.5 bits), Expect = 7.2e-60, Sum P(2) = 7.2e-60
Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTSS 118
DYWGQGT++TVSS

Sbjct: 108 DYWGQGTTLTVSS 120

>gp|M36216|MUSIGHADW_1 immunoglobulin heavy chain V-region [Mus musculus]
Length = 120

Score = 409 (185.9 bits), Expect = 7.2e-60, Sum P(2) = 7.2e-60
Identities = 80/117 (68%), Positives = 93/117 (79%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQSGAELVR G SVK+SCKASGYT T+Y + WVKQ PG GLEWIG+I+PG G T Y

Sbjct: 1 QVQLQQSGAELVRPGTSVKISCKASGYTFTNYWLGWVKQRPQHGLEWIGDIYPGGGYTNY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTVTS 117
N+KFKGKA+LTADTSSSTAYMQ+SSLTSEDSAVYFCAR + + + G T++

Sbjct: 61 NEKFKGKATLTADTSSSTAYMQLSSLTSEDSAVYFCARSVYYGGSYYFDYWGQGTTLT 117

Score = 65 (29.5 bits), Expect = 7.2e-60, Sum P(2) = 7.2e-60
Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTSS 118
DYWGQGT++TVSS

Sbjct: 108 DYWGQGTTLTVSS 120

>gp|L25855|MUSIGGB_1 IgG gene product [Mus musculus]
Length = 119

Score = 407 (185.0 bits), Expect = 7.3e-60, Sum P(2) = 7.3e-60
Identities = 76/98 (77%), Positives = 85/98 (86%)

Query: 4 LQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYYNQK 63
LQQSGAELV+ GASVK+SCK SGYT T Y + W+KQ P QGL WIG IFPG G TYYN+K

Sbjct: 4 LQQSGAELVKPGASVKLSCKTSGYTFTRYWIKQRPQGLGWIGEIFPGTGTTYNEK 63

Query: 64 FKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNW 101
FKGKA+LT DTSSSTAYMQ+SSLTSEDSAVYFCARG++

Sbjct: 64 FKGKATLTIDTSSSTAYMQLSSLTSEDSAVYFCARGDY 101

Score = 67 (30.5 bits), Expect = 7.3e-60, Sum P(2) = 7.3e-60
Identities = 12/16 (75%), Positives = 14/16 (87%)

Query: 103 GALDYWGQGTSTVTVSS 118
G DYWGQGT++TVSS
Sbjct: 104 GQEDYWGQGTTLTVSS 119

>gp|S77022|S77022_1 anti-CD29 antibody heavy chain variable region [Mus sp.]
Length = 116

Score = 403 (183.2 bits), Expect = 7.5e-60, Sum P(2) = 7.5e-60
Identities = 74/97 (76%), Positives = 86/97 (88%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQ+SG ELVR GASVK+SCKASGYT T Y + WVKQ PGQGLEWI I+PG+G+T+Y
Sbjct: 1 QVQLQESGTELVRPGASVKLSCKASGYTFTDYYISWVKQRPQGLEWIARIYPGSGNTFY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCA 97
N+KFKGKA+LTA+TSS+TAYMQ+SSLTSEDSAVYFCA
Sbjct: 61 NEKFKGKATLTAETSSNTAYMQLSSLTSEDSAVYFCA 97

Score = 71 (32.3 bits), Expect = 7.5e-60, Sum P(2) = 7.5e-60
Identities = 13/16 (81%), Positives = 15/16 (93%)

Query: 103 GALDYWGQGTSTVTVSS 118
G+ DYWGQGT+VTVSS
Sbjct: 101 GSGDYWGQGTTVTVSS 116

>gp|M36225|MUSIGHAEF_1 immunoglobulin heavy chain V-region [Mus musculus]
Length = 118

Score = 468 (212.8 bits), Expect = 9.9e-60, P = 9.9e-60
Identities = 92/118 (77%), Positives = 99/118 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQSGAEL + GASVKMSCKASGYT TSY MHWVKQ PGQGLEWIG I P G T Y
Sbjct: 1 QVQLQQSGAELAKPGASVKMSCKASGYTFTSYWMHWVKQRPQGLEWIGYINPSTGYTEY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTVTVSS 118
NQKFK KA+LTAD SSSTAYMQ+SSLTSEDSA+Y+CAR + A+DYWGQGTSTVTVSS
Sbjct: 61 NQKFKDKATLTADKSSSTAYMQLSSLTSEDSALYYCARWVYYYAMDYWGQGTSTVTVSS 118

>pir|S40295|S40295 Ig gamma-2a chain (mAb735) - mouse
Length = 446

Score = 420 (190.9 bits), Expect = 1.1e-59, Sum P(2) = 1.1e-59
Identities = 79/99 (79%), Positives = 88/99 (88%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQSG ELVR GASVK+SCKASGYT T Y +HWVKQ PG+GLEWIG I+PG+G+T Y
Sbjct: 1 QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEWIGWIYPGSGNTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARG 99
N+KFKGKA+LT DTSSSTAYMQ+SSLTSEDSAVYFCARG
Sbjct: 61 NEKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARG 99

Score = 77 (35.0 bits), Expect = 1.1e-59, Sum P(2) = 1.1e-59
Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTVSS 118
A+DYWGQGTSTVTVSS
Sbjct: 103 AMDYWGQGTSTVTVSS 117

>gp|L22749|MUSI_1 immunoglobulin heavy chain [Mus musculus]
Length = 118

Score = 467 (212.3 bits), Expect = 1.4e-59, P = 1.4e-59
Identities = 89/118 (75%), Positives = 101/118 (85%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYMMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQSGAELVR G SVKMSCKA+GYT T+Y + WVKQ PG GLEWIG+I+PG G T Y
Sbjct: 1 QVQLQQSGAELVRPGTSVKMSCKAAGYTFITNYWIGWVKRPGHGLEWIGDIYPGGGYTNY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTVSS 118
N+KFKGKA+LTADTSSSTAYMQ+SSLTSEDSA+Y+CAR + A+DYWGQGTSTVSS
Sbjct: 61 NEKFKGKATLTADTSSSTAYMQLSSLTSEDSAIYYCARPFYFAMDYWGQGTSTVSS 118

>gp|M61026|MUSIGHAANN_1 immunoglobulin heavy chain VDJ region [Mus musculus]
Length = 118

Score = 467 (212.3 bits), Expect = 1.4e-59, P = 1.4e-59
Identities = 89/118 (75%), Positives = 99/118 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYMMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQ GAELV+ GASVK+SCKASGYT TSY MMHWVK PG+GLEWIG I P +G T Y
Sbjct: 1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYLMMHWVKRPGRGLEWIGRIDPNSGGTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTVSS 118
N+KFK KA+LT D SSTAYMQ+SSLTSEDSAVY+CAR + GA+DYWGQGTSTVSS
Sbjct: 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYYYGGAMDYWGQGTSTVSS 118

>gp|M31287|MUSIGHAVA_1 IgG gene product [Mus musculus]
Length = 115

Score = 466 (211.8 bits), Expect = 1.9e-59, P = 1.9e-59
Identities = 88/115 (76%), Positives = 96/115 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYMMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
+ LQQSG L R GASVKMSCKASGYT TSY MMHWVK PGQGLEWIG I+PGN DT Y
Sbjct: 1 EVQLQQSGTVLARPASVKMSCKASGYTFTSYMMHWVKRPGQGLEWIGAIYPGNSDTRY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTV 115
NQKFKGKA LTA TS+STAYM++SSLT+EDSAVY+C RG A+DYWGQGTSTV
Sbjct: 61 NQKFKGKAKLTAVTSASTAYMELSSLTNEEDSAVYYCTRGLFTAMDYWGQGTSTV 115

>gp|M31288|MUSIGHAWA_1 Mouse active rheumatoid factor IgA chain (family J558)
mRNA J4 region, partial cds, hybridoma AM15. [Mus musculus]
Length = 115

Score = 466 (211.8 bits), Expect = 1.9e-59, P = 1.9e-59
Identities = 88/115 (76%), Positives = 96/115 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYMMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
+ LQQSG L R GASVKMSCKASGYT TSY MMHWVK PGQGLEWIG I+PGN DT Y
Sbjct: 1 EVQLQQSGTVLARPASVKMSCKASGYTFTSYMMHWVKRPGQGLEWIGAIYPGNSDTSY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTV 115
NQKFKGKA LTA TS+STAYM++SSLT+EDSAVY+C RG A+DYWGQGTSTV
Sbjct: 61 NQKFKGKAKLTAVTSASTAYMELSSLTNEEDSAVYYCTRGLFTAMDYWGQGTSTV 115

>gp|M31908|MUSIGHRC_1 Mouse Ig H-chain V-D-J region mRNA, from hybridoma
hVH65-211, partial cds. [Mus musculus]
Length = 121

Score = 404 (183.7 bits), Expect = 2.5e-59, Sum P(2) = 2.5e-59
Identities = 77/103 (74%), Positives = 86/103 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYMMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
+ LQQSGAELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG Y
Sbjct: 1 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKRPGQGLEWIGYINPGNGYIKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEG 103
 N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR + G
 Sbjct: 61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSEYYG 103

Score = 66 (30.0 bits), Expect = 2.5e-59, Sum P(2) = 2.5e-59
 Identities = 11/15 (73%), Positives = 14/15 (93%)

Query: 104 ALDYWGQGTSTVTVSS 118
 + DYWGQGT++TVSS
 Sbjct: 107 SFDYWGQGTTLTVSS 121

>gp|M36226|MUSIGHAEG_1 immunoglobulin heavy chain V-region [Mus musculus]
 Length = 120

Score = 414 (188.2 bits), Expect = 2.5e-59, Sum P(2) = 2.5e-59
 Identities = 79/99 (79%), Positives = 87/99 (87%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQSGAELVR G SVK+SCKASGYT T+Y + WVKQ PG GLEWIG+I+PG G T Y
 Sbjct: 1 QVQLQQSGAELVRPGTSVKISCKASGYTFTNYWLGWVKQRPQGHGLEWIGDIYPGGGYTNY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG 99
 N+KFKGKA+LTADTSSSTAYMQ+SSLTSEDSAVYFCARG
 Sbjct: 61 NEKFKGKATLTADTSSSTAYMQLSSLTSEDSAVYFCARG 99

Score = 56 (25.5 bits), Expect = 2.5e-59, Sum P(2) = 2.5e-59
 Identities = 10/12 (83%), Positives = 11/12 (91%)

Query: 107 YWGQGTSTVTVSS 118
 YWGQGT VTVS+
 Sbjct: 109 YWGQGTTLTVSA 120

>gp|U36491|MMU36491_1 J558+ IgM heavy chain [Mus musculus]
 Length = 109

Score = 402 (182.7 bits), Expect = 2.8e-59, Sum P(2) = 2.8e-59
 Identities = 75/95 (78%), Positives = 81/95 (85%)

Query: 7 SGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYYNQKFKG 66
 SG ELV+ GASVK+SCKASGYT TSY MHWVKQ PGQGLEWIGNI P NG T YN+KFK
 Sbjct: 1 SGTSLVPGASVKLSCKASGYTFTSYNMHWVKQRPQGLEWIGNINPNSGGTNYNEKFKS 60

Query: 67 KASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 101
 KA+LT D SSSTAYMQ+SSLTSEDSAVY+CAR W
 Sbjct: 61 KATLTVDKSSSTAYMQLSSLTSEDSAVYFCARSGW 95

Score = 68 (30.9 bits), Expect = 2.8e-59, Sum P(2) = 2.8e-59
 Identities = 12/16 (75%), Positives = 14/16 (87%)

Query: 103 GALDYWGQGTSTVTVSS 118
 G DYWGQGT++TVSS
 Sbjct: 94 GWFYWGQGTTLTVSS 109

>gp|L35315|MUSIVDJA_1 immunoglobulin heavy chain [Mus musculus]
 Length = 143

Score = 404 (183.7 bits), Expect = 2.9e-59, Sum P(2) = 2.9e-59
 Identities = 77/98 (78%), Positives = 83/98 (84%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQ G ELV+ GASVK+SCKASGYT TSY MHWVKQ PGQGLEWIGNI P NG T Y
 Sbjct: 20 QVQLQQPGTELKPGASVKLSCKASGYTFTSYNMHWVKQRPQGLEWIGNINPNSGGTNY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR 98
 N+KFK KA+LT D SSSTAYMQ+SSLTSEDSAVY+CAR

Sbjct: 80 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR 117

Score = 65 (29.5 bits), Expect = 2.9e-59, Sum P(2) = 2.9e-59
Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTVSS 118
DYWGQGT++TVSS

Sbjct: 128 DYWGQGTTLTVSS 140

>gp|X88902|MMVARHECH_1 Fv fragment variable heavy chain [Mus musculus]
Length = 131

Score = 389 (176.8 bits), Expect = 3.2e-59, Sum P(2) = 3.2e-59
Identities = 75/95 (78%), Positives = 83/95 (87%)

Query: 4 LQSGAELVRSGASVKMSCKASGYTLTSYMMHWVKQTPGQGLEWIGNIFPGNGDTYYNQK 63
LQ+SGA LV+ GASVKMSCKASGYT TSY MHWVKQ PGQGLEWIG I P N T YN+K

Sbjct: 4 LQESGAGLVKPGASVKMSCKASGYTFTSYMMHWVKQKPGQGLEWIGYINPYNDGTYNEK 63

Query: 64 FKGKASLTADTSSSTAYMQISLTSSEDSAVYFCAR 98
FKGKA+LT+D SSSTAYM++SSLTSEDSAVY+CAR

Sbjct: 64 FKGKATLTSDKSSSTAYMELSSLTSEDSAVYFCAR 98

Score = 80 (36.4 bits), Expect = 3.2e-59, Sum P(2) = 3.2e-59
Identities = 14/18 (77%), Positives = 16/18 (88%)

Query: 101 WEGALDYWGQGTSTVTVSS 118
W A+DYWGQGT+VTVSS

Sbjct: 105 WYYAMDYWGQGTTVTVSS 122

WARNING: HSPs involving 8585 database sequences were not reported due to the limiting value of parameter B = 50.

Parameters:

V=100

B=50

H=1

-qtype

E=10

-ctxfactor=1.00

Query	Frame	MatID	Matrix name	----- Lambda	As Used K	----- H	----- Lambda	Computed K	----- H
+0	0	BLOSUM62	0.315	0.127	0.386	same	same	same	

Query	Frame	MatID	Length	Eff.Length	E	S	W	T	X	E2	S2
+0	0	118	118	10.59	3	11	22	0.18	31		

Statistics:

Query	Frame	MatID	Expected High Score	Observed High Score	HSPs Reportable	HSPs Reported
+0	0	63 (28.6 bits)	542 (246.4 bits)	17989	94	

Query	Frame	MatID	Neighborhd Words	Word Hits	Excluded Hits	Failed Extensions	Successful Extensions	Overlaps Excluded
+0	0	3523	12605070	3175944	9368862	60214	834	

Database: Non-redundant PDB+SwissProt+SPupdate+PIR+GenPept+GPupdate

Release date: 5:56 AM EST Jan 19, 1996

Posted date: 5:57 AM EST Jan 19, 1996

of letters in database: 51,001,589

of sequences in database: 172,206

of database sequences satisfying E: 8635

No. of states in DFA: 546 (54 KB)

Total size of DFA: 92 KB (128 KB)

11D10 Heavy Chain PEPTIDE - 21

Time to generate neighborhood: 0.02u 0.01s 0.03t Real: 00:00:00
No. of processors used: 8
Time to search database: 82.38u 1.48s 83.86t Real: 00:00:17
Total cpu time: 82.47u 1.53s 84.00t Real: 00:00:18

WARNINGS ISSUED: 2

S. Chatterjee

```
===== 1121
Return-Path: <blastmai@BLASTER.NLM.NIH.GOV>
Received: from UKCC (NJE origin SMTP@UKCC) by UKCC.UKY.EDU (LMail V1.2a/1.8a) with BSMTP id 5094; Fri,
19 Jan 1996 16:19:56 -0500
Received: from ncbi.nlm.nih.gov by UKCC.uky.edu (IBM VM SMTP V2R3) with TCP;
Fri, 19 Jan 96 16:19:54 EST
Received: from blaster.nlm.nih.gov by ncbi.nlm.nih.gov
id QAA16046; Fri, 19 Jan 1996 16:19:43 -0500
Received: by blaster.nlm.nih.gov (950511.SGI.8.6.12.PATCH526/5.6)
id QAA21085; Fri, 19 Jan 1996 16:19:43 -0500
Date: Fri, 19 Jan 1996 16:19:43 -0500
Message-Id: <199601192119.QAA21085@blaster.nlm.nih.gov>
To: SKCHAT00@UKCC.uky.edu
Subject: Results-BLAST Server
From: NCBI BLAST E-Mail Server <blast@ncbi.nlm.nih.gov>
Errors-To: <owner-blast@ncbi.nlm.nih.gov>
Reply-To: "NCBI BLAST E-Mail Server" <blast@ncbi.nlm.nih.gov>
```

```
==+=====
To Obtain Documentation: send an e-mail message to 'blast@ncbi.nlm.nih.gov'
with the word HELP in the body of the message. The documentation was last
modified March 18th.
```

```
==+=====
March 18, 1995
The BLAST FAQ was updated with the question Q33 related to degenerated
nucleotide code available for the BLAST programs.
```

```
==+=====
August 8, 1995
A new server directive ACKNOWLEDGE, has been added to the server. See the
help file for more details.
```

```
Trying blaster... connected
National Center for Biotechnology Information (NCBI)
```

Experimental GENINFO(R) BLAST Network Service (Blaster)

Fri Jan 19 16:16:50 EST 1996, Up 30 days, 4:08, 0 user, load: 14.58, 13.81, 14.79

PEPTIDE SEQUENCE DATABASES

```
nr Non-redundant PDB+SwissProt+PIR+SPUpdate+GenPept+GPUUpdate, updated daily
for efficient, complete searches of the five component databases:
pdb Brookhaven Protein Data Bank, April 1995 Release
swissprot SWISS-PROT Release 32.0, December 1995
pir PIR Release 45.0 (complete), June 30, 1995
spupdate SWISS-PROT cumulative weekly update to the major release
genpept CDS translations from GenBank(R) Release 92, December 15, 1995
gpupdate cumulative daily updates to the major release of genpept
kabatpro Kabat Sequences of Proteins of Immunological Interest, June 1995
tfd TFD transcription factor (protein) database Release 7.0, June 1993
alu * Translations of select Alu repeats from REPBASE
```

NUCLEOTIDE SEQUENCE DATABASES

```
nr Non-redundant PDB+GBUpdate+GenBank+EmblUpdate+EMBL, updated daily
for efficient, complete searches of the four component databases:
pdb Brookhaven Protein Data Bank, April 1995 Release
genbank GenBank(R) Release 92 (no daily updates), December 15, 1995
gbupdate GenBank(R) cumulative daily updates to the major release
embl EMBL Data Library, Release 45.0, December 1995
emblu EMBL Data Library cumulative daily updates to the major release
vector Vector subset of GenBank(R), February 3rd, 1995
alu ** Select Alu repeats from REPBASE
kbatnuc Kabat Sequences of Nucleic Acid of Immunological Interest, June 1995
epd Eukaryotic Promoter Database Release 43, June 1995
dbest + Database of Expressed Sequence Tags (cumulative daily update)
dbsts + Database of Sequence Tagged Sites Release 1.5, October 26, 1994
```


[illegible]

22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 10

[illegible][illegible]

0.016	3864	27	:
0.010	3837	22	:
0.0063	3815	19	:
0.0040	3796	28	:
0.0025	3768	20	:
0.0016	3748	13	:

			High	Smallest	
			Score	Sum	
Sequences producing High-scoring Segment Pairs:			Probability	P(N)	N
gp L41880 MUSIKCC_1	immunoglobulin kappa chain [Mus mu...	491	4.7e-63	1	
gp J00550 MUSIGKAC2_1	immunoglobulin kappa chain variabl...	486	2.1e-62	1	
sp P01639 KV5G_MOUSE	IG KAPPA CHAIN PRECURSOR V-V REGIO...	486	2.3e-62	1	
gp V00808 MMIGK7_1	immunoglobulin kappa [Mus musculus]	481	1.1e-61	1	
pir PL0260 PL0260	Ig kappa chain V region (anti-DNA,...	481	1.4e-61	1	
gp M59920 MUSIGKAA3_1	Ig kappa chain [Mus musculus]	480	1.9e-61	1	
pir PL0259 PL0259	Ig kappa chain V region (anti-DNA,...	477	4.8e-61	1	
gp Z22118 MDIGKVBS_1	immunoglobulin variable region [Mu...	461	7.5e-59	1	
gp M36246 MUSIGLAFA_1	immunoglobulin kappa-chain VK-1 [M...	455	5.3e-58	1	
pdb 2GFB A	Igg2a Fab Fragment (Cnj206) >pdb 2...	447	3.1e-57	1	
gp M64168 MUSIGKAF1_1	immunoglobulin kappa-chain VK-1 [M...	446	9.0e-57	1	
pir PL0262 PL0262	Ig kappa chain V region (anti-DNA,...	439	7.9e-56	1	
gp X02177 MMIGGVJ1_1	Immunoglobulin G kappa light chain...	431	8.3e-55	1	
gp U25098 MMU25098_1	immunoglobulin light chain [Mus mu...	430	1.3e-54	1	
gp V00804 MMIGK3_1	kappa-immunoglobulin [Mus musculus...	427	3.2e-54	1	
gp U29617 MMU29617_1	Ig kappa chain [Mus musculus]	427	3.9e-54	1	
gp X02178 MMIGGVJ2_1	immunoglobulin G kappa light chain...	426	4.0e-54	1	
pir B47271 B47271	nitrophenyl phosphonate-specific a...	425	6.4e-54	1	
gp M12191 MUSIGKCMA_1	Mouse Ig active kappa-chain VJ2C m...	419	3.6e-53	1	
pir PH1062 PH1062	Ig light chain V region (clone 202...	415	1.7e-52	1	
gp S69053 S69053_1	anti-p-nitrophenyl phosphonate est...	415	1.7e-52	1	
pir PL0261 PL0261	Ig kappa chain V region (anti-DNA,...	399	2.9e-50	1	
gp U30236 MMU30236_1	Ig kappa chain [Mus musculus]	396	6.7e-50	1	
gp U19320 MMU19320_1	immunoglobulin kappa light chain v...	396	6.8e-50	1	
pir C28840 C28840	Ig kappa chain V region (HP22) - m...	387	1.1e-48	1	
pir B28840 B28840	Ig kappa chain V region (HP27) - m...	387	1.1e-48	1	
gp X03382 MMIGKGA1_1	Mouse mRNA for GAT (HP27) anti-idi...	387	1.1e-48	1	
gp X03383 MMIGKGA2_1	Mouse mRNA for GAT (HP22) anti-idi...	386	1.6e-48	1	
pir D32513 D32513	Ig kappa chain precursor V region ...	385	1.6e-48	1	
gp U20061 MMU20061_1	immunoglobulin kappa chain [Mus mu...	381	7.0e-48	1	
gp M33559 MUSIGKABE_1	Mouse Ig rearranged kappa-chain mR...	381	7.0e-48	1	
pir PL0220 PL0220	Ig kappa chain V region (G) - mous...	371	1.7e-46	1	
pir D28840 D28840	Ig kappa chain V region (HP29) - m...	371	1.9e-46	1	
gp J00568 MUSIGKAE_1	mouse ig kappa unproductively rear...	369	2.6e-46	1	
gp S76654 S76654_1	F30C7 light chain variable region ...	368	4.3e-46	1	
gp M36261 MUSIGLAFF_1	immunoglobulin kappa-chain VK-1 [M...	367	5.8e-46	1	
gp X55042 MMIGKL221_1	immunoglobulin kappa light chain [...	300	6.6e-46	2	
sp P01641 KV5H_MOUSE	IG KAPPA CHAIN PRECURSOR V-V REGIO...	365	1.0e-45	1	
pir JL0080 JL0080	Ig light chain precursor V region ...	365	1.0e-45	1	
pir A38740 A38740	Ig kappa chain V region (Py20) - m...	365	1.1e-45	1	
sp P01643 KV5J_MOUSE	IG KAPPA CHAIN V-V REGION (MOPC 17...	365	1.1e-45	1	
gp X55044 MMIGKL229_1	immunoglobulin kappa light chain [...	365	1.1e-45	1	
gp U21066 MMU21066_1	immunoglobulin kappa chain variabl...	365	1.3e-45	1	
gp U16180 MMU16180_1	Ig light chain [Mus musculus]	364	1.5e-45	1	
gp Z37332 HSIGVKC45_1	immunoglobulin kappa light chain v...	300	1.6e-45	2	
gp M36236 MUSIGLAEQ_1	immunoglobulin kappa-chain VK-1 [M...	363	2.1e-45	1	
gp X55047 MMIGKL4A1_1	immunoglobulin kappa light chain [...	300	2.3e-45	2	
pir S38862 S38862	Ig kappa chain V region - mouse >g...	299	4.3e-45	2	
gp L35316 MUSIVJR_1	immunoglobulin light chain [Mus mu...	360	4.4e-45	1	
gp U16689 MMU16689_1	immunoglobulin light chain precurs...	360	4.5e-45	1	
pdb 2F19 L	Fab Fragment From A Monoclonal Ant...	358	5.0e-45	1	
pdb 6FAB L	Antigen-Binding Fragment Of The Mu...	358	5.0e-45	1	
pir E38740 E38740	Ig kappa chain V region (Py54) - m...	360	5.1e-45	1	
gp X55041 MMIGKL218_1	immunoglobulin kappa light chain [...	360	5.3e-45	1	
gp M14840 MUSIGKBP_1	Mouse IgM monoclonal anti-BrMRBC a...	360	5.3e-45	1	
sp P01644 KV5K_MOUSE	IG KAPPA CHAIN V-V REGION (HP R16...	359	7.2e-45	1	

gp M34593 MUSIGKABW_1	Mouse Ig kappa-chain mRNA V-J regi...	359	7.2e-45	1
gp M15519 MUSIGKCM_1	Mouse allele 91A3 V-region kappa c...	358	8.4e-45	1
pdb 1FBI L	Fab Fragment Of The Monoclonal Ant...	356	9.4e-45	1
pir G38740 G38740	Ig kappa chain V region (Py69) - m...	358	9.7e-45	1
sp P01648 KV50_MOUSE	IG KAPPA CHAIN V-V REGION (HP 91A3).	358	9.9e-45	1
gp S77030 S77030_1	H4-specific antibody light chain v...	358	9.9e-45	1
pir PH1224 PH1224	Ig kappa chain precursor V region ...	357	1.2e-44	1
gp X53329 MMHS2H1VL_1	2H1 VL gene product [Mus musculus]	357	1.2e-44	1
sp P01646 KV5M_MOUSE	IG KAPPA CHAIN V-V REGION (HP 123E6).	357	1.4e-44	1
sp P01647 KV5N_MOUSE	IG KAPPA CHAIN V-V REGION (HP 124E1).	357	1.4e-44	1
pir C26405 C26405	Ig kappa chain V region (3D10) - m...	357	1.4e-44	1
pir S19970 S19970	Ig kappa chain V region (M-T151) - ...	357	1.4e-44	1
gp M32043 MUSIGKCR_1	Mouse Ig kappa-chain mRNA V-J regi...	357	1.4e-44	1
pir S32188 S32188	Ig kappa chain V region - mouse (f...	357	1.4e-44	1
gp L01279 HUMIGKVCA_1	immunoglobulin kappa chain [Homo s...	297	1.5e-44	2
gp U05217 MMU05217_1	anti-platelet integrin gpIIb/IIIa ...	356	1.6e-44	1
gp X06111 MMIGKVJ2_1	Mouse (hVH65-107) mRNA for immunog...	356	1.9e-44	1
gp X05796 MMIGVK36_1	immunoglobulin L chain [Mus muscul...	356	1.9e-44	1
gp M31915 MUSIGKCRO_1	Mouse Ig light-chain V-J region mR...	356	1.9e-44	1
pir B28044 B28044	Ig kappa chain V region (GP1) - mouse	356	1.9e-44	1
gp M37021 MUSIGKADT_1	Mouse Ig rearranged kappa-chain mR...	356	1.9e-44	1
gp M36242 MUSIGKAEW_1	immunoglobulin kappa-chain VK-1 [M...	356	1.9e-44	1
gp M15402 RATIGKAC_1	Rat Ig active kappa-chain mRNA VJ-...	355	2.0e-44	1
pir B23986 B23986	Ig kappa chain precursor V region ...	355	2.1e-44	1
pir A34904 A34904	Ig kappa chain precursor V region ...	355	2.2e-44	1
pir A29380 A29380	Ig kappa chain precursor V region ...	355	2.3e-44	1
pir C38740 C38740	Ig kappa chain V region (Py2) - mouse	355	2.5e-44	1
pir PL0282 PL0282	Ig light chain V region (45-49, an...	355	2.6e-44	1
gp M34590 MUSIGKABT_1	Mouse Ig kappa-chain mRNA V-J regi...	355	2.6e-44	1
gp M32040 MUSIGKCRQ_1	Mouse Ig kappa-chain mRNA V-J regi...	355	2.6e-44	1
gp S74560 S74560_1	rheumatoid factor RF3-2C [Mus sp.]	355	2.6e-44	1
gp M59918 MUSIGKAA1_1	Ig kappa chain [Mus musculus] >gp ...	354	2.9e-44	1
pir A26406 A26406	Ig kappa chain V region (Ars-A) - ...	354	3.0e-44	1
sp P01645 KV5L_MOUSE	IG KAPPA CHAIN V-V REGION (HP 93G7).	354	3.5e-44	1
pir B26405 B26405	Ig kappa chain V region (1F6) - mouse	354	3.5e-44	1
pir B30551 B30551	Ig kappa chain V region (36-71) - ...	354	3.5e-44	1
gp M33678 MUSIGKABF_1	Mouse Ig rearranged L-chain mRNA V...	354	3.5e-44	1
gp M60020 MUSIGKAAAM_1	Ig kappa chain [Mus musculus]	353	4.1e-44	1
gp X72463 HSIGKLV42_1	Ig kappa light chain (VJC) [Homo s...	353	4.1e-44	1
pir S40353 S40353	Ig kappa light chain (VJC) - human.	353	4.2e-44	1
gp L39092 MUSIGK527A_1	anti-fluorescein antibody [Mus mus...	352	5.7e-44	1
pir B48677 B48677	Ig light chain V-J region (44.1) - ...	352	6.7e-44	1
gp M36256 MUSIGLAFK_1	immunoglobulin kappa-chain VK-1 [M...	352	6.7e-44	1
gp S77025 S77025_1	H2A/H2B-specific antibody light ch...	352	6.7e-44	1

WARNING: Descriptions of 5103 database sequences were not reported due to the limiting value of parameter V = 100.

>gp|L41880|MUSIKCC_1 immunoglobulin kappa chain [Mus musculus]
Length = 130

Score = 491 (223.7 bits), Expect = 4.7e-63, P = 4.7e-63
Identities = 99/107 (92%), Positives = 102/107 (95%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLSGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSLSGSGVPK
Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLDGSGVPK 82

Query: 61 RFGSGSRSGSDYSLTISSLESDFVAYYCLQYASSPYTFGGGKLEIK 107
RFGSGSRSGSDYSLTISSLES DFV YYCLQYASSPYTFGGGKLEIK
Sbjct: 83 RFGSGSRSGSDYSLTISSLESEDFVYYCLQYASSPYTFGGGKLEIK 129

>gp|J00550|MUSIGKAC2_1 immunoglobulin kappa chain variable region [Mus musculus]
Length = 146

Score = 486 (221.4 bits), Expect = 2.1e-62, P = 2.1e-62
Identities = 98/107 (91%), Positives = 102/107 (95%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPK 82

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGSRSGSDYSLTISSLES DFV YYCLQYASSP+TFGGGKLEIK
Sbjct: 83 RFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGGGKLEIK 129

>sp|P01639|KV5G_MOUSE IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 41).
>pir|A93211|KVMSM4 Ig kappa chain precursor V region (MOPC 41) -
mouse
Length = 130

Score = 486 (221.4 bits), Expect = 2.3e-62, P = 2.3e-62
Identities = 98/107 (91%), Positives = 102/107 (95%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPK 82

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGSRSGSDYSLTISSLES DFV YYCLQYASSP+TFGGGKLEIK
Sbjct: 83 RFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGGGKLEIK 129

>gp|V00808|MMIGK7_1 immunoglobulin kappa [Mus musculus]
Length = 130

Score = 481 (219.1 bits), Expect = 1.1e-61, P = 1.1e-61
Identities = 97/107 (90%), Positives = 101/107 (94%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCR SQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRPSQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPK 82

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGSRSGSDYSLTISSLES DFV YYCLQYASSP+TFGGGKLEIK
Sbjct: 83 RFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGGGKLEIK 129

>pir|PL0260|PL0260 Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
Length = 106

Score = 481 (219.1 bits), Expect = 1.4e-61, P = 1.4e-61
Identities = 97/106 (91%), Positives = 101/106 (95%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
Sbjct: 1 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPK 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEI 106
RFSGSRSGSDYSLTISSLES DFV YYCLQYASSP+TFGGGKLEI
Sbjct: 61 RFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGGGKLEI 106

>gp|M59920|MUSIGKAA3_1 Ig kappa chain [Mus musculus]
Length = 107

Score = 480 (218.7 bits), Expect = 1.9e-61, P = 1.9e-61
Identities = 97/106 (91%), Positives = 101/106 (95%)

Query: 2 IQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKR 61
IQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPKR
Sbjct: 1 IQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPKR 60

Query: 62 FSGSRSGSDYSLTISLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
 FSGSRSGSDYSLTISLES DFV YYCLQYASSP+TFGGGKLEIK
 Sbjct: 61 FSGSRSGSDYSLTISSESEDFVDYYCLQYASSPWTFGGGKLEIK 106

>pir|PL0259|PL0259 Ig kappa chain V region (anti-DNA, DP11VK) - mouse
 (fragment)
 Length = 106

Score = 477 (217.3 bits), Expect = 4.8e-61, P = 4.8e-61
 Identities = 96/106 (90%), Positives = 101/106 (95%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
 Sbjct: 1 DIQMTQSPSSLSASLGERVSLTCRASQDIGRSLNLWQQEPDGTIKRLIYATSSLD SGVPK 60

Query: 61 RFSGRSGSDYSLTISLESQDFVAYYCLQYASSPYTFGGGKLEI 106
 RFSGRSGSDYSLTISLES DFV YYCLQYA+SP+TFGGGKLEI
 Sbjct: 61 RFSGRSGSDYSLTISSESEDFVDYYCLQYATSPWTFGGGKLEI 106

>gp|Z22118|MDIGKVB5_1 immunoglobulin variable region [Mus musculus domesticus]
 Length = 107

Score = 461 (210.0 bits), Expect = 7.5e-59, P = 7.5e-59
 Identities = 93/107 (86%), Positives = 98/107 (91%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIY+TS+L SGVPK
 Sbjct: 1 DIQMTQSPSSLSASLGERVSLTCRASQEI SGYLSWLQQKPDGTIKRLIYSTSTLNSGVPK 60

Query: 61 RFSGRSGSDYSLTISLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFSGRSGSDYSLTISLES DF YYCLQYASSPYTFGGGKLEIK
 Sbjct: 61 RFSGRSGSDYSLTISSESEDFADYYCLQYASSPYTFGGGKLEIK 107

>gp|M36246|MUSIGLAFA_1 immunoglobulin kappa-chain VK-1 [Mus musculus]
 Length = 101

Score = 455 (207.3 bits), Expect = 5.3e-58, P = 5.3e-58
 Identities = 92/101 (91%), Positives = 95/101 (94%)

Query: 7 SPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGR 66
 SPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPKRFSGR
 Sbjct: 1 SPSSLSASLGERVSLTCRASQDIGSSNLWQQEPDGTIKRLIYATSSLD SGVPKRFSGR 60

Query: 67 SGSDYSLTISLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
 SGSDYSLTISLES DFV YYCLQYASSPYTFGGGKLEIK
 Sbjct: 61 SGSDYSLTISSESEDFVDYYCLQYASSPYTFGGGKLEIK 101

>pdb|2GFB|A Igg2a Fab Fragment (Cnj206) >pdb|2GFB|C Igg2a Fab Fragment (Cnj206)
 >pdb|2GFB|E Igg2a Fab Fragment (Cnj206) >pdb|2GFB|G Igg2a Fab
 Fragment (Cnj206) >pdb|2GFB|I Igg2a Fab Fragment (Cnj206)
 >pdb|2GFB|K Igg2a Fab Fragment (Cnj206) >pdb|2GFB|M Igg2a Fab
 Fragment (Cnj206) >pdb|2GFB|O Igg2a Fab Fragment (Cnj206)
 Length = 214

Score = 447 (203.6 bits), Expect = 3.1e-57, P = 3.1e-57
 Identities = 91/105 (86%), Positives = 95/105 (90%)

Query: 2 IQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKR 61
 IQMTQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIYA S+L SGVPKR
 Sbjct: 2 IQMTQSPSSLSASLGERVSLTCRASQEI SGYLSWLQQKPDGTIKRLIYAASLD SGVPKR 61

Query: 62 FSGSRSGSDYSLTISLESQDFVAYYCLQYASSPYTFGGGKLEI 106
 FSGSRSGSDYSLTISLES DF YYCLQYASSPYTFGGGKLEI
 Sbjct: 62 FSGSRSGSDYSLTISSESEDFADYYCLQYASSPYTFGGGKLEI 106

>gp|M64168|MUSIGKFT_1 immunoglobulin kappa-chain VK-1 [Mus musculus]
Length = 102

Score = 446 (203.2 bits), Expect = 9.0e-57, P = 9.0e-57
Identities = 90/101 (89%), Positives = 94/101 (93%)

Query: 7 SPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSR 66
SPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPKRFSGSR
Sbjct: 2 SPSSLSASLGERVSLTCRASQDIGNSLNWLQQEPDGTIKRLIYATSSLDSGVPKRFSGSR 61

Query: 67 SGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGTKLEIK 107
SGSDYSLTISSLES DFV YYCLQYAS YTFGGGTKLE+K
Sbjct: 62 SGSDYSLTISSLESEDFVYYCLQYASYTTYTFGGGTKLELK 102

>pir|PL0262|PL0262 Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
Length = 106

Score = 439 (200.0 bits), Expect = 7.9e-56, P = 7.9e-56
Identities = 89/106 (83%), Positives = 94/106 (88%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQ+IG L LQQ+PDGTIKRLIYA S+L SGVPK
Sbjct: 1 DIQMTQSPSSLSASLGERVSLACRASQEIIGGYLSWLQQKPDGTIKRLIYAASLD SGVPK 60

Query: 61 RFSGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGTKLEI 106
RF GSRSGSDYSLTISSLES DF YYCLQYAS P+TFGGGTKLEI
Sbjct: 61 RFSGSRSGSDYSLTISSLESEDFADYYCLQYASYPTFGGGTKLEI 106

>gp|X02177|MMIGGVJ1_1 Immunoglobulin G kappa light chain [Mus musculus]
Length = 126

Score = 431 (196.4 bits), Expect = 8.3e-55, P = 8.3e-55
Identities = 88/107 (82%), Positives = 93/107 (86%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIYA S+L SGVPK
Sbjct: 14 DIQMTQSPSSLSASLGERVSLTCRASQEI SGYLSWLQQKPDGTIKRLIYAASLD SGVPK 73

Query: 61 RFSGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGTKLEIK 107
RFSGSRSGSDYSLTISSLES DF YYCLQY S P TFG GTKLE+K
Sbjct: 74 RFSGSRSGSDYSLTISSLESEDFADYYCLQYLSYPLTFGAGTKLELK 120

>gp|U25098|MMU25098_1 immunoglobulin light chain [Mus musculus]
Length = 112

Score = 430 (195.9 bits), Expect = 1.3e-54, P = 1.3e-54
Identities = 87/107 (81%), Positives = 94/107 (87%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
++QMTQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIYA S+L SGVPK
Sbjct: 1 ELQMTQSPSSLSASLGERVSLTCRASQEI SGYLSWLQQKPDGTIKRLIYAASLD SGVPK 60

Query: 61 RFSGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGTKLEIK 107
RFSGSRSGSDYSLTISSLES DF YYCLQYAS P TFG GTKLE+K
Sbjct: 61 RFSGSRSGSDYSLTISSLESEDFADYYCLQYASYPLTFGAGTKLELK 107

>gp|V00804|MMIGK3_1 kappa-immunoglobulin [Mus musculus] >gp|J00566|MUSIGKVC_1
Mouse ig kappa germline v gene: vk41. [Mus musculus]
Length = 117

Score = 427 (194.5 bits), Expect = 3.2e-54, P = 3.2e-54
Identities = 87/95 (91%), Positives = 90/95 (94%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
 Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLDGSGVPK 82

Query: 61 RFGSRSGSDYSLTISSLESGDFVAYYCLQYASSP 95
 RFGSRSGSDYSLTISSLES DFV YYCLQYASSP
 Sbjct: 83 RFGSRSGSDYSLTISSLESEDFVDYYCLQYASSP 117

>gp|U29617|MMU29617_1 Ig kappa chain [Mus musculus]
 Length = 95

Score = 427 (194.5 bits), Expect = 3.9e-54, P = 3.9e-54
 Identities = 87/95 (91%), Positives = 90/95 (94%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
 Sbjct: 1 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLDGSGVPK 60

Query: 61 RFGSRSGSDYSLTISSLESGDFVAYYCLQYASSP 95
 RFGSRSGSDYSLTISSLES DFV YYCLQYASSP
 Sbjct: 61 RFGSRSGSDYSLTISSLESEDFVDYYCLQYASSP 95

>gp|X02178|MMIGGVJ2_1 immunoglobulin G kappa light chain [Mus musculus]
 Length = 127

Score = 426 (194.1 bits), Expect = 4.0e-54, P = 4.0e-54
 Identities = 87/107 (81%), Positives = 92/107 (85%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIYA S+L SGVPK
 Sbjct: 15 DIQMTQSPSSLSASLGERVSLTCRASQEI SGYLSWLQQKPDGTIKRLIYAASLDGSGVPK 74

Query: 61 RFGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFGSRSGSDYSLTISSLES DF YYCLQY S P TFG GTKLE+K
 Sbjct: 75 RFGSRSGSDYSLTISSLESEDFADYYCLQYLSYPLTFGAGTKLEIK 121

>pir|B47271|B47271 nitrophenyl phosphonate-specific antibody 48G7 light chain
 VJ - Escherichia coli (fragment) >gp|S55170|S55170_1 nitrophenyl
 phosphonate-specific antibody 48G7 light chain VJ [Mus sp.]
 Length = 108

Score = 425 (193.6 bits), Expect = 6.4e-54, P = 6.4e-54
 Identities = 87/107 (81%), Positives = 94/107 (87%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 ++ +TQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIYA S+L SGVPK
 Sbjct: 2 ELVLTQSPSSLSASLGERVSLTCRASQEI NGYLGWLQQKPDGTIKRLIYAASLDHSGVPK 61

Query: 61 RFGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFGSRSGSDYSLTISSLES DF YYCLQYAS P TFGGGKLEIK
 Sbjct: 62 RFGSRSGSDYSLTISSLESEDFADYYCLQYASYPRTFGGGKLEIK 108

>gp|M12191|MUSIGKMA_1 Mouse Ig active kappa-chain VJ2C mRNA from plasmacytoma
 MOPC 173B, partial cds. [Mus musculus]
 Length = 127

Score = 419 (190.9 bits), Expect = 3.6e-53, P = 3.6e-53
 Identities = 87/107 (81%), Positives = 91/107 (85%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQDI L+ QQ+P TIK LIY TS+L SGVPK
 Sbjct: 17 DIQMTQSPSSLSASLGERVSLTCRASQDI HGYNLFQQKPGETIKHLIYETSNLDGSGVPK 76

Query: 61 RFGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFGSRSGSDYSL I SLES DF YYCLQYASSP TFGGGKLEIK

Sbjct: 77 RFSGSRSGSDYSLIIGSLESEDFADYYCLQYASSPPTFGGGTKLEIK 123

>pir|PH1062|PH1062 Ig light chain V region (clone 202.105) - mouse (fragment)
Length = 98

Score = 415 (189.1 bits), Expect = 1.7e-52, P = 1.7e-52
Identities = 84/98 (85%), Positives = 89/98 (90%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIY+TS+L SGVPK
Sbjct: 1 DIQMTQSPSSLSASLGERVSLTCRASQEISGYLSWLQQKPDGTIKRLIYSTSTLNSGVPK 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTF 98
RFSGSRSGSDYSLTISSLES DF YYCLQYASSPYTF
Sbjct: 61 RFSGSRSGSDYSLTISSLESEDFADYYCLQYASSPYTF 98

>gp|S69053|S69053_1 anti-p-nitrophenyl phosphonate esterolytic antibody kappa
chain variable region [Mus sp.]
Length = 98

Score = 415 (189.1 bits), Expect = 1.7e-52, P = 1.7e-52
Identities = 84/98 (85%), Positives = 88/98 (89%)

Query: 8 PSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSRS 67
PSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIYA S+L SGVPKRFSGSRS
Sbjct: 1 PSSLSASLGERVSLTCRASQEISGYLSWLQQKPDGTIKRLIYAASLD SGVPKRFSGSRS 60

Query: 68 GSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGTKLE 105
GSDYSLTISSLES DF YYCLQYASSPYTFGGGTKLE
Sbjct: 61 GSDYSLTISSLESEDFADYYCLQYASSPYTFGGGTKLE 98

>pir|PL0261|PL0261 Ig kappa chain V region (anti-DNA, DP15VK) - mouse
(fragment)
Length = 88

Score = 399 (181.8 bits), Expect = 2.9e-50, P = 2.9e-50
Identities = 80/88 (90%), Positives = 83/88 (94%)

Query: 19 VSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSL 78
VSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPKRFSGSRSGSDYSLTISSL
Sbjct: 1 VSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPKRFSGSRSGSDYSLTISSL 60

Query: 79 ESGDFVAYYCLQYASSPYTFGGGTKLEI 106
ES DFV YYCLQYASSP+TFGGGTKLEI
Sbjct: 61 ESEDFVDYYCLQYASSPWTFGGGTKLEI 88

>gp|U30236|MMU30236_1.Ig kappa chain [Mus musculus]
Length = 98

Score = 396 (180.4 bits), Expect = 6.7e-50, P = 6.7e-50
Identities = 81/93 (87%), Positives = 86/93 (92%)

Query: 4 MTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFS 63
MTQ+PSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPKRFS
Sbjct: 4 MTQTPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPKRFS 63

Query: 64 GSRSGSDYSLTISSLESQDFVAYYCLQYASSPY 96
GSRSGSDYSLT SSLES DFV Y CLQYASSP+
Sbjct: 64 GSRSGSDYSLTSSSLESEDFVDYSLQYASSPW 96

>gp|U19320|MMU19320_1 immunoglobulin kappa light chain variable region [Mus
musculus]
Length = 97

Score = 396 (180.4 bits), Expect = 6.8e-50, P = 6.8e-50
Identities = 81/97 (83%), Positives = 85/97 (87%)

Query: 9 SSSLASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSRSG 68
SSLSASLG+RVSLTCRASQ+I L LQ+PDGTIKRLIYA S+L SGVPKRFSGSRSG
Sbjct: 1 SSSLASLGERVSLTCRASQEISGYLSWLQKPDGTIKRLIYAASLTDSGVPKRFSGSRSG 60

Query: 69 SDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLE 105
SDYSLTISSLES DF YYCLQYAS PYTFG GTKLE
Sbjct: 61 SDYSLTISSLESEDFADYYCLQYASPYTFGGGKLE 97

>pir|C28840|C28840 Ig kappa chain V region (HP22) - mouse (fragment)
Length = 101

Score = 387 (176.3 bits), Expect = 1.1e-48, P = 1.1e-48
Identities = 79/101 (78%), Positives = 86/101 (85%)

Query: 7 SPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSR 66
S SSSLSA LG+R LTCRASQDI + L+ LQ++ DGTIKRLIY+TS+L SGVPKRFSGSR
Sbjct: 1 SLSSLSAXLGERXXLTTCRASQDISVYLNWLQRKLDGTIKRLIYSTSTLDSGVPKRFSGSR 60

Query: 67 SGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
SG DYSLTISSLES DF Y CLQYASSPYTFGGGK EIK
Sbjct: 61 SGLDYSLTISSLESEDFADYXCLQYASSPYTFGGGKXEIK 101

>pir|B28840|B28840 Ig kappa chain V region (HP27) - mouse (fragment)
Length = 101

Score = 387 (176.3 bits), Expect = 1.1e-48, P = 1.1e-48
Identities = 79/100 (79%), Positives = 87/100 (87%)

Query: 7 SPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSR 66
S SSSLSA LG+R SLTCRASQDI + L+ LQ++ DGTIKRLIY+TS+L SGVPKRFSGSR
Sbjct: 1 SLSSLSATLGERDSLTCRASQDISVYLNWLQRKLDGTIKRLIYSTSTLDSGVPKRFSGSR 60

Query: 67 SGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEI 106
SG DYSLTISSLES DF YYCLQYASSPYTFGGGK I
Sbjct: 61 SGLDYSLTISSLESEDFADYXCLQYASSPYTFGGGKXXI 100

>gp|X03382|MMIGKA1_1 Mouse mRNA for GAT (HP27) anti-idiotypic Ab2 Ig (k) light
chain against public idiotopes GAT antigen = Glu(60)Ala(30)Tyr(10)
co-polymer. [Mus musculus]
Length = 100

Score = 387 (176.3 bits), Expect = 1.1e-48, P = 1.1e-48
Identities = 79/100 (79%), Positives = 87/100 (87%)

Query: 7 SPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSR 66
S SSSLSA LG+R SLTCRASQDI + L+ LQ++ DGTIKRLIY+TS+L SGVPKRFSGSR
Sbjct: 1 SLSSLSATLGERDSLTCRASQDISVYLNWLQRKLDGTIKRLIYSTSTLDSGVPKRFSGSR 60

Query: 67 SGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEI 106
SG DYSLTISSLES DF YYCLQYASSPYTFGGGK I
Sbjct: 61 SGLDYSLTISSLESEDFADYXCLQYASSPYTFGGGKXXI 100

>gp|X03383|MMIGKA2_1 Mouse mRNA for GAT (HP22) anti-idiotypic Ab2 Ig (k) light
chain against public idiotopes GAT antigen = Glu(60)Ala(30)Tyr(10)
co-polymer. [Mus musculus]
Length = 99

Score = 386 (175.9 bits), Expect = 1.6e-48, P = 1.6e-48
Identities = 78/99 (78%), Positives = 85/99 (85%)

Query: 9 SSSLASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSRSG 68
SSLSA LG+R /LTCRASQDI + L+ LQ++ DGTIKRLIY+TS+L SGVPKRFSGSRSG

Sbjct: 1 SSLSAXLGERXXLTCRASQDISVYLNWLQQRKLDGTIKRLIYSTSTLDSGVPKRFGSGSRSG 60

Query: 69 SDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
DYSLTISSLES DF Y CLQYASSPYTFGGGK EIK

Sbjct: 61 LDYSLTISSLESEDFADYXCLQYASSPYTFGGGTXEIK 99

>pir|032513|032513 Ig kappa chain precursor V region (BXW16) - mouse
>gp|M20832|MUSIGKCLN_1 Mouse IgMk rearranged kappa light-chain mRNA
variable region (V-J-kappa) anti-DNA autoantibody. [Mus musculus]
Length = 129

Score = 385 (175.4 bits), Expect = 1.6e-48, P = 1.6e-48
Identities = 80/107 (74%), Positives = 86/107 (80%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLSGSGVPK 60
DIQM QSPSS+ SLG RVSL+CRASQ I NL QQ+P GTIK LIY+TS+L SGVP
Sbjct: 23 DIQMIQSPSSMFGSLGDRVSLSCRASQGIRGNLDWYQQKPGGTIKLLIYSTSNLNSGVPS 82

Query: 61 RFGSGRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFGSGS SGGDYSLTISSLES DF YYCLQ + PYTFGGGKLEIK
Sbjct: 83 RFGSGSGSDYSLTISSLESEDFADYYCLQRNAYPYTFGGGKLEIK 129

>gp|U20061|MMU20061_1 immunoglobulin kappa chain [Mus musculus]
Length = 108

Score = 381 (173.6 bits), Expect = 7.0e-48, P = 7.0e-48
Identities = 80/107 (74%), Positives = 86/107 (80%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLSGSGVPK 60
DIQM QSPSS+ ASLG RVSL+CRASQ I NL QQ+P GTIK LIY+TS+L SGVP
Sbjct: 1 DIQMIQSPSSMFASLGDRVSLSCRASQGIRGNLDWYQQKPGGTIKLLIYSTSNLNSGVPS 60

Query: 61 RFGSGRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFGSGS SGGDYSLTISSLES DF YYCLQ + P TFGGGKLEIK
Sbjct: 61 RFGSGSGSDYSLTISSLESEDFADYYCLQRNAYPLTFGGGKLEIK 107

>gp|M33559|MUSIGKABE_1 Mouse Ig rearranged kappa-chain mRNA V-J2-region,
hybridoma A6.1, partial cds. [Mus musculus]
Length = 107

Score = 381 (173.6 bits), Expect = 7.0e-48, P = 7.0e-48
Identities = 80/107 (74%), Positives = 86/107 (80%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLSGSGVPK 60
DIQM QSPSS+ ASLG RVSL+CRASQ I NL QQ+P GTIK LIY+TS+L SGVP
Sbjct: 1 DIQMIQSPSSMFASLGDRVSLSCRASQGIRGNLDWYQQKPGGTIKLLIYSTSNLNSGVPS 60

Query: 61 RFGSGRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFGSGS SGGDYSLTISSLES DF YYCLQ + P TFGGGKLEIK
Sbjct: 61 RFGSGSGSDYSLTISSLESEDFADYYCLQRNAYPLTFGGGKLEIK 107

>pir|PLO220|PLO220 Ig kappa chain V region (G) - mouse (fragment)
>pir|B49026|B49026 Ab2 kappa chain V region, mAb G=monoclonal
auto-anti-idiotypic - mouse
Length = 107

Score = 371 (169.0 bits), Expect = 1.7e-46, P = 1.7e-46
Identities = 75/107 (70%), Positives = 85/107 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLSGSGVPK 60
DIQMTQ+ SSLSASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP
Sbjct: 1 DIQMTQTSSLSASLGDRVTISCRASQDISVYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Query: 61 RFGSGRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFGSGS SG+DYSLTIS+LE D YYC QY+ P TFGGGKLEIK

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Sbjct: 61 RFSGSGSGTDYSLTISNLEPEDIATYYCQYSKLPRTFGGGTKLEIK 107

>pir|D28840|D28840 Ig kappa chain V region (HP29) - mouse (fragment)
 >gp|X03384|MMIGKGA3_1 Mouse mRNA for GAT (HP29) anti-idiotypic Ab2
 Ig (k) light chain against public idiotopes GAT antigen =
 Glu(60)Ala(30)Tyr(10) co-polymer. [Mus musculus]
 Length = 92

Score = 371 (169.0 bits), Expect = 1.9e-46, P = 1.9e-46
 Identities = 73/92 (79%), Positives = 82/92 (89%)

Query: 16 GQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGRSGSDYSLTI 75
 G+R SLTCRASQDI + L+ LQQ+ DGTIKRLIY+TS L SGVPKRFSGRSG+DYSLTI
 Sbjct: 1 GERESLTCRASQDISVYLNWLQKLDGTIKRLIYSTILD SGVPKRFSGRSGTDYSLTI 60

Query: 76 SSLESGDFVAYYCLQYASSPYTFGGGKLEIK 107
 +SLES DF Y+CLQYASSP+TFGGGKLEIK
 Sbjct: 61 NSLESEDFADYFCLQYASSPFTFGGGKLEIK 92

>gp|J00568|MUSIGKAE_1 mouse ig kappa unproductively rearranged gene: mopc173b
 v-j region. [Mus musculus]
 Length = 127

Score = 369 (168.1 bits), Expect = 2.6e-46, P = 2.6e-46
 Identities = 78/101 (77%), Positives = 82/101 (81%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQDI L+ QQ+P TIK LIY TS+L SGVPK
 Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRASQDIHGYNLFQKKPGETIKHLIYETSNLD SGVPK 82

Query: 61 RFSGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGG 101
 RFSGSRSGSDYSL I SLES DF YYCLQYASSP GG
 Sbjct: 83 RFSGSRSGSDYSLTIISLESEDFADYCLQYASSPPRSEGG 123

>gp|S76654|S76654_1 F30C7 light chain variable region [Mus sp.]
 Length = 107

Score = 368 (167.7 bits), Expect = 4.3e-46, P = 4.3e-46
 Identities = 74/107 (69%), Positives = 85/107 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQS SLSASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP
 Sbjct: 1 DIQMTQSSSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFSGS SG+DYSLTIS+LE D YYC QY++ P TFG GTKLE+K
 Sbjct: 61 RFSGSGSGTDYSLTISNLEPEDIATYYCQYSNLPLTFGAGTKLELK 107

>gp|M36261|MUSIGLAFF_1 immunoglobulin kappa-chain VK-1 [Mus musculus]
 Length = 107

Score = 367 (167.2 bits), Expect = 5.8e-46, P = 5.8e-46
 Identities = 74/107 (69%), Positives = 85/107 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQ+ SLSASLG RV+++C ASQ I L+ QQ+PDGT+K LIY TSSL SGVP
 Sbjct: 1 DIQMTQTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFSGS SG+DYSLTIS+LE D YYC QY+ P+TFGGGKLEIK
 Sbjct: 61 RFSGSGSGTDYSLTISNLEPEDIATYYCQYSKLPWTFGGGKLEIK 107

>gp|X55042|MMIGKL221_1 immunoglobulin kappa light chain [Mus musculus]
 >gp|M63609|MUSIGKAVB_1 immunoglobulin kappa chain [Mus musculus]

Length = 107

Score = 300 (136.7 bits), Expect = 6.6e-46, Sum P(2) = 6.6e-46
Identities = 61/90 (67%), Positives = 71/90 (78%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQ+ SLSASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP
Sbjct: 1 DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTSSLESQDFVAYYCLQ 90
RFSGS SG+DYSLTIS+LE D Y+C Q
Sbjct: 61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQ 90

Score = 71 (32.3 bits), Expect = 6.6e-46, Sum P(2) = 6.6e-46
Identities = 14/24 (58%), Positives = 18/24 (75%)

Query: 84 VAYYCLQYASSPYTFGGGKLEIK 107
+A Y Q ++ +TFGGGKLEIK
Sbjct: 83 IATYFCQQGNTLWTFGGGKLEIK 106

>sp|P01641|KV5H_MOUSE IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 173B).
>pi|A01924|KVMS3B Ig kappa chain precursor V region (VKM173B) -
mouse >gp|K00880|MUSIGKVE_1 mouse ig kappa germline v gene:
mopc173b. [Mus musculus]
Length = 117

Score = 365 (166.3 bits), Expect = 1.0e-45, P = 1.0e-45
Identities = 76/95 (80%), Positives = 80/95 (84%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQDI L+ QQ+P TIK LIY TS+L SGVPK
Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRASQDIGYLNLFQQKPGETIKHLIYETSNDLDSGVPK 82

Query: 61 RFSGSRSGSDYSLTSSLESQDFVAYYCLQYASSP 95
RFSGSRSGSDYSL I SLES DF YYCLQYASSP
Sbjct: 83 RFSGSRSGSDYSLIIGSLESEDFADYYCLQYASSP 117

>pi|JL0080|JL0080 Ig light chain precursor V region (anti-phenyloxazolone,
18C10) - mouse (fragment) >gp|M27793|MUSIGKCPW_1 Mouse Ig active
kappa-chain mRNA V-J5 region, clone 18C10. [Mus musculus]
Length = 115

Score = 365 (166.3 bits), Expect = 1.0e-45, P = 1.0e-45
Identities = 74/107 (69%), Positives = 85/107 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQ+ SLSASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP
Sbjct: 7 DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 66

Query: 61 RFSGSRSGSDYSLTSSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGS SG+DYSLTIS+LE D Y+C Q + PYTFGGGKLEIK
Sbjct: 67 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGKLEIK 113

>pi|A38740|A38740 Ig kappa chain V region (Py20) - mouse
Length = 111

Score = 365 (166.3 bits), Expect = 1.1e-45, P = 1.1e-45
Identities = 73/107 (68%), Positives = 85/107 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
D+QMTQ+ SLSASLG RV+++C ASQ I L+ QQ+PDGT+K LIY TSSL SGVP
Sbjct: 4 DVQMTQTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 63

Query: 61 RFSGSRSGSDYSLTSSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGS SG+DYSLTIS+LE D YYC QY+ P+TFGGGKLEIK
Sbjct: 64 RFSGSGSGTDYSLTISNLEPEDVATYYCQYKVPWTFGGGKLEIK 110

>sp|P01643|KV5J_MOUSE IG KAPPA CHAIN V-V REGION (MOPC 173). >pir|A01926|KVMS73
Ig kappa chain V region (MOPC 173) - mouse
Length = 108

Score = 365 (166.3 bits), Expect = 1.1e-45, P = 1.1e-45
Identities = 73/107 (68%), Positives = 83/107 (77%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQ+ SSSLASLG RV+++C ASQ IG L QQ+PDGT+K LIY TSSL SGVP
Sbjct: 1 DIQMTQTSSLSASLGDRVTISCSASQSIGNYLWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGS SG+DYSLTIS L+ + YYC QY+ P TFGGGKLEIK
Sbjct: 61 RFSGSGSGTDYSLTISBLZPZBIATYYCQYQSKLPRTFGGGKLEIK 107

>gp|X55044|MMIGKL229_1 immunoglobulin kappa light chain [Mus musculus]
>gp|X55045|MMIGKL233_1 immunoglobulin kappa light chain [Mus
musculus] >gp|X55046|MMIGKL38_1 immunoglobulin kappa light chain
[Mus musculus] >gp|M63611|MUSIGKAVD_1 immunoglobulin kappa chain
[Mus musculus] >gp|M63612|MUSIGKAVE_1 immunoglobulin kappa chain
[Mus musculus] >gp|M63613|MUSIGKAVF_1 immunoglobulin kappa chain
[Mus musculus]
Length = 108

Score = 365 (166.3 bits), Expect = 1.1e-45, P = 1.1e-45
Identities = 74/107 (69%), Positives = 85/107 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQ+ SSSLASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP
Sbjct: 1 DIQMTQTSSLSASLGDRVTISCRASQDISNYLWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGS SG+DYSLTIS+LE D Y+C Q + PYTFGGGKLEIK
Sbjct: 61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGKLEIK 107

>gp|U21066|MMU21066_1 immunoglobulin kappa chain variable and joining regions
[Mus musculus]
Length = 90

Score = 365 (166.3 bits), Expect = 1.3e-45, P = 1.3e-45
Identities = 73/88 (82%), Positives = 77/88 (87%)

Query: 16 GQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTI 75
G++ CRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPKRFSGSRSGSDYSLTI
Sbjct: 3 GRKSQSHCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPKRFSGSRSGSDYSLTI 62

Query: 76 SSLESQDFVAYYCLQYASSPYTFGGGK 103
SSLES DFV YYCLQYA SPYTFG GTK
Sbjct: 63 SSLESEDFVDYYCLQYAFSPYTFGSGTK 90

>gp|U16180|MMU16180_1 Ig light chain [Mus musculus]
Length = 107

Score = 364 (165.8 bits), Expect = 1.5e-45, P = 1.5e-45
Identities = 77/107 (71%), Positives = 84/107 (78%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQM QSPSS+ A LG RVS +CRASQ NL QQ+P GTIK LIY+TS+L SGVP
Sbjct: 1 DIQMIQSPSSMFAFLGDRVSPSCRASQGRGNLDWYQQKPGGTIKLLIYSTSNLKSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGS SGSDYSLTIS+LES DF YYCLQ + PYTFGGGKLEIK
Sbjct: 61 RFSGSGSGSDYSLTISTLESEDFADYYCLQRNAFPYTFGGGKLEIK 107

>gp|Z37332|HSIGVKC45_1 immunoglobulin kappa light chain variable region [Homo sapiens]
Length = 117

Score = 300 (136.7 bits), Expect = 1.6e-45, Sum P(2) = 1.6e-45
Identities = 64/101 (63%), Positives = 74/101 (73%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSAS+G RV++TCRASQ I L+ QQ+P K LIYA SSL SGVP
Sbjct: 1 DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGG 101
RFSGS SG+D++LTISSL+ DF YYC Q S+P GG
Sbjct: 61 RFSGSGSGTDFLTISLQPEDFATYYCQSYSTPPLTFGG 101

Score = 68 (31.0 bits), Expect = 1.6e-45, Sum P(2) = 1.6e-45
Identities = 12/17 (70%), Positives = 15/17 (88%)

Query: 91 YASSPYTFGGGKLEIK 107
Y++ P TFGGK+EIK
Sbjct: 92 YSTPPLTFGGGKVEIK 108

>gp|M36236|MUSIGLAEQ_1 immunoglobulin kappa-chain VK-1 [Mus musculus]
Length = 105

Score = 363 (165.4 bits), Expect = 2.1e-45, P = 2.1e-45
Identities = 73/105 (69%), Positives = 83/105 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQ+ SSLSASLG RV+++C ASQ I L+ QQ+PDGT+K LIY TSSL SGVP
Sbjct: 1 DIQMTQTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLE 105
RFSGS SG+DYSLTIS+LE D YYC QY+ PYTFGGGKLE
Sbjct: 61 RFSGSGSGTDYSLTISNLEPEDIATYYCQYQSKLPYTFGGGKLE 105

>gp|X55047|MMIGKL4A1_1 immunoglobulin kappa light chain [Mus musculus]
>gp|M63674|MUSIGKAVG_1 immunoglobulin kappa chain [Mus musculus]
>gp|M63616|MUSIGKAVI_1 immunoglobulin kappa chain [Mus musculus]
Length = 107

Score = 300 (136.7 bits), Expect = 2.3e-45, Sum P(2) = 2.3e-45
Identities = 61/90 (67%), Positives = 71/90 (78%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQ+ SSLSASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP
Sbjct: 1 DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQ 90
RFSGS SG+DYSLTIS+LE D Y+C Q
Sbjct: 61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQ 90

Score = 67 (30.5 bits), Expect = 2.3e-45, Sum P(2) = 2.3e-45
Identities = 14/24 (58%), Positives = 17/24 (70%)

Query: 84 VAYYCLQYASSPYTFGGGKLEIK 107
+A Y Q ++ TFGGKLEIK
Sbjct: 83 IATYFCQQGNTLRTFGGKLEIK 106

>pir|S38862|S38862 Ig kappa chain V region - mouse >gp|X75854|MMIGKC1_1
immunoglobulin variable kappa light chain [Mus musculus]
Length = 108

Score = 299 (136.2 bits), Expect = 4.3e-45, Sum P(2) = 4.3e-45
Identities = 62/101 (61%), Positives = 75/101 (74%)

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Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60

D+QMTQ+ SSL+ASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP

Sbjct: 1 DVQMTQTSSLAASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSESGDFVAYYCLQYASSPYTFGGG 101

RFSGS SG+DYSLTIS+LE D Y+C Q + P GG

Sbjct: 61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPPWTFGG 101

S. Chatterjee

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===== 2006
Return-Path: <blastmai@BLASTER.NLM.NIH.GOV>
Received: from UKCC (NJE origin SMTP@UKCC) by UKCC.UKY.EDU (LMail V1.2a/1.8a) with BSMTTP id 2242; Fri,
19 Jan 1996 17:16:15 -0500
Received: from ncbi.nlm.nih.gov by UKCC.uky.edu (IBM VM SMTP V2R3) with TCP;
Fri, 19 Jan 96 17:16:12 EST
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Date: Fri, 19 Jan 1996 17:15:57 -0500
Message-Id: <199601192215.RAA04498@blaster.nlm.nih.gov>
To: SKCHAT00@UKCC.uky.edu
Subject: Results-BLAST Server
From: NCBI BLAST E-Mail Server <blast@ncbi.nlm.nih.gov>
Errors-To: <owner-blast@ncbi.nlm.nih.gov>
Reply-To: "NCBI BLAST E-Mail Server" <blast@ncbi.nlm.nih.gov>

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To Obtain Documentation: send an e-mail message to 'blast@ncbi.nlm.nih.gov'
with the word HELP in the body of the message. The documentation was last
modified March 18th.
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March 18, 1995
The BLAST FAQ was updated with the question Q33 related to degenerated
nucleotide code available for the BLAST programs.
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August 8, 1995
A new server directive ACKNOWLEDGE, has been added to the server. See the
help file for more details.
-----

```

Trying blaster... connected
National Center for Biotechnology Information (NCBI)

Experimental GENINFO(R) BLAST Network Service (Blaster)

Fri Jan 19 17:14:36 EST 1996, Up 30 days, 5:05, 1 user, load: 22.91, 24.88, 20.67

PEPTIDE SEQUENCE DATABASES

```

nr Non-redundant PDB+SwissProt+PIR+SPUUpdate+GenPept+GUPUpdate, updated daily
for efficient, complete searches of the five component databases:
  pdb      Brookhaven Protein Data Bank, April 1995 Release
  swissprot SWISS-PROT Release 32.0, December 1995
  pir      PIR Release 45.0 (complete), June 30, 1995
  spuupdate SWISS-PROT cumulative weekly update to the major release
  genpept   CDS translations from GenBank(R) Release 92, December 15, 1995
  gupupdate cumulative daily updates to the major release of genpept
  kabatpro  Kabat Sequences of Proteins of Immunological Interest, June 1995
  tfd      TFD transcription factor (protein) database Release 7.0, June 1993
  alu *    Translations of select Alu repeats from REPBASE

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NUCLEOTIDE SEQUENCE DATABASES

```

nr Non-redundant PDB+GBUpdate+GenBank+EmblUpdate+EMBL, updated daily
for efficient, complete searches of the four component databases:
  pdb      Brookhaven Protein Data Bank, April 1995 Release
  genbank   GenBank(R) Release 92 (no daily updates), December 15, 1995
  gbupdate  GenBank(R) cumulative daily updates to the major release
  embl      EMBL Data Library, Release 45.0, December 1995
  emblu     EMBL Data Library cumulative daily updates to the major release
  vector    Vector subset of GenBank(R), February 3rd, 1995
  alu **    Select Alu repeats from REPBASE
  kabatnuc  Kabat Sequences of Nucleic Acid of Immunological Interest, June 1995
  epd       Eukaryotic Promoter Database Release 43, June 1995
  dbest +   Database of Expressed Sequence Tags (cumulative daily update)
  dbsts +   Database of Sequence Tagged Sites Release 1.5, October 26, 1994

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* Databases that are not accessible through the NCBI Retrieve E-mail server.
+ The TBLASTX program is restricted to searching these databases.

You can obtain the BLAST documentation files, send a message consisting of just the word "help" (without the quotes) to: blast@ncbi.nlm.nih.gov
Last modification dates: August 10th 95 for the E-mail server help, January 19th 94 for the BLAST manual and March 18th 95 for the BLAST FAQ.

For a free subscription to "NCBI News", the NCBI newsletter, send a request along with your name and postal mailing address to: info@ncbi.nlm.nih.gov

A new GenBank sequence submission tool, called BankIt, is now available through the NCBI's home page on the World Wide Web. The URL is <http://www.ncbi.nlm.nih.gov/>

BLASTN 1.4.8MP (20-June-1995) (Build 08:41:09 Oct 19 1995)

Reference: Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990). Basic local alignment search tool. *J. Mol. Biol.* 215:403-10.

Notice: this program and its default parameter settings are optimized to find nearly identical sequences rapidly. To identify weak similarities encoded in nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= 11D10VL.nuc
(321 letters)

Database: Non-redundant PDB+GBupdate+GenBank+EMBLupdate+EMBL
662,343 sequences; 449,479,361 total letters.

Searching.....done

Observed Numbers of Database Sequences Satisfying Various EXPECTation Thresholds (E parameter values)

Histogram units: = 4 Sequences : less than 4 sequences

EXPECTation Threshold
(E parameter)

[illegible]

0.10	3155	10	==
0.063	3145	4	=
0.040	3141	5	=
0.025	3136	8	==
0.016	3128	7	=
0.010	3121	6	=
0.0063	3115	7	=
0.0040	3108	3	:
0.0025	3105	2	:
0.0016	3103	2	:

Sequences producing High-scoring Segment Pairs:			High Score	Smallest Sum Probability P(N)	N
gb L41880	MUSIKCC	Mus musculus immunoglobulin kappa c...	1533	2.4e-122	1
gb L48667	MUSX	Mus musculus (cell line C3H/F2-15) ...	1517	6.3e-121	1
gb J00565	MUSIGKAC1	Mouse ig kappa active gene: vk41 v-...	1488	7.7e-119	1
emb V00808	MMIGK7	Part of the murine gene for kappa-i...	1479	4.3e-118	1
gb I03643	I03643	Sequence 4 from patent US 4642334. ...	1479	9.1e-118	1
gb M59920	MUSIGKAA3	Mouse Ig germline chain mRNA V-J re...	1464	1.6e-116	1
gb M36246	MUSIGLAFA	Mouse Ig kappa-chain mRNA V region,...	1445	6.6e-115	1
emb Z22118	MDIGKVBS	M.domesticus IgK variable region.	1434	5.1e-114	1
gb M64168	MUSIGKAF	Mouse Ig active kappa-chain mRNA V-...	1407	9.4e-112	1
emb X02177	MMIGGVJ1	M.musculus mRNA for IgG kappa light...	1362	4.2e-108	1
gb U29617	MMU29617	Mus musculus anti-DNA antibody Ig k...	1357	1.5e-107	1
gb J00566	MUSIGKVC	Mouse ig kappa germline v gene: vk4...	1351	2.0e-107	1
gb U25098	MMU25098	Mus musculus anti-Pseudomonas aerug...	1353	2.7e-107	1
emb X02178	MMIGGVJ2	M.musculus mRNA for IgG kappa light...	1335	7.4e-106	1
emb X63811	MMVKMRB11	M.musculus mRNA for IgM V(k)MRB11	1332	1.8e-105	1
gb M12191	MUSIGKCA	Mouse Ig active kappa-chain VJ2C mR...	1326	4.1e-105	1
gb S69053	S69053	Ig V kappa =anti-p-nitrophenyl phos...	1326	5.3e-105	1
gb U30236	MMU19326	Mus musculus anti-DNA antibody Ig k...	1297	1.4e-102	1
gb S55170	S55170	nitrophenyl phosphonate-specific an...	1290	4.8e-102	1
emb X03382	MMIGKGA1	Mouse mRNA for GAT (HP27) anti-idio...	1289	6.2e-102	1
gb J00568	MUSIGKAE	mouse ig kappa unproductively rearr...	1177	7.2e-101	2
gb U19320	MMU19320	Mus musculus immunoglobulin kappa l...	1276	7.7e-101	1
emb X03383	MMIGKGA2	Mouse mRNA for GAT (HP22) anti-idio...	1270	2.4e-100	1
gb U21066	MMU21066	Mus musculus immunoglobulin kappa c...	1121	1.3e-98	2
gb L22571	MUSIGKAF2	Mouse IgK chain mRNA V-region.	557	1.5e-97	5
gb M20832	MUSIGKCLN	Mouse IgMk rearranged kappa light-c...	1200	1.2e-94	1
gb U20061	MMU20061	Mus musculus anti-DNA antibody immu...	1191	8.2e-94	1
gb M33559	MUSIGKABE	Mouse Ig rearranged kappa-chain mRN...	1191	8.3e-94	1
gb K00880	MUSIGKVE	mouse ig kappa germline v gene: mop...	1180	1.3e-91	1
gb U16180	MMU16180	Mus musculus anti-cardiolipin antib...	1137	2.6e-89	1
emb X03384	MMIGKGA3	Mouse mRNA for GAT (HP29) anti-idio...	1137	3.0e-89	1
gb U19327	MMU19327	Mus musculus immunoglobulin kappa l...	1129	1.5e-88	1
gb U19326	MMU19326	Mus musculus immunoglobulin kappa l...	1086	5.9e-85	1
gb M36236	MUSIGLAEQ	Mouse Ig kappa-chain mRNA V region,...	1027	3.7e-80	1
gb M84436	MUSIGLBM	Mouse rearranged light chain variab...	1011	7.0e-79	1
gb M27793	MUSIGKCPW	Mouse Ig active kappa-chain mRNA V-...	1011	7.3e-79	1
gb M63611	MUSIGKAVD	Mouse Ig rearranged kappa-chain (V-...	1011	7.7e-79	1
gb M63609	MUSIGKAVB	Mouse Ig rearranged kappa-chain (V-...	832	2.6e-78	2
gb U20820	MMU20820	Mus musculus Ig Fab F9.13.7 light c...	993	2.4e-77	1
gb M36261	MUSIGLAFF	Mouse Ig kappa-chain mRNA V region,...	993	2.5e-77	1
gb M63614	MUSIGKAVG	Mouse Ig rearranged kappa-chain (V-...	832	8.0e-77	2
emb X70090	MMNL4H10	M.musculus NL4H10 mRNA for immunogl...	986	9.4e-77	1
gb M60020	MUSIGKAAAM	Mouse Ig kappa chain mRNA V-J regio...	984	1.1e-76	1
gb S50261	S50261	Ig VL=anti-CD4 mAb M-T151 variable ...	984	1.2e-76	1
gb M84440	MUSIGLCC	Mouse rearranged light chain variab...	984	1.2e-76	1
emb X65095	MMIGLCL151	M.musculus mRNA for IG light chain ...	984	1.4e-76	1
gb S76654	S76654	Ig VL=F30C7 light chain variable re...	984	1.4e-76	1
gb M36242	MUSIGLAEW	Mouse Ig kappa-chain mRNA V region,...	979	3.6e-76	1
emb X85995	HSDELIGVJ	H.sapiens mRNA for immunoglobulin k...	975	6.4e-76	1
gb M84434	MUSIGLAC	Mouse rearranged light chain variab...	975	6.9e-76	1
gb S74560	S74560	Ig V kappa =rheumatoid factor RF3-2...	973	1.1e-75	1
gb K00745	MUSIGKAAO	Mouse Ig kappa active V-region: ant...	965	5.2e-75	1

gb	L35316	MUSIVJR	Mus musculus germline immunoglobuli...	957	2.0e-74	1
gb	M84442	MUSIGLCH	Mouse rearranged light chain variab...	957	2.2e-74	1
gb	M63608	MUSIGKAVA	Mouse Ig rearranged kappa-chain (V-...	957	2.4e-74	1
gb	S77025	S77025	Ig VL=H2A/H2B-specific antibody lig...	952	6.3e-74	1
gb	S63022	S63022	anti-ganglioside GD3 immunoglobulin...	948	1.1e-73	1
gb	M60019	MUSIGKAAAL	Mouse Ig kappa chain mRNA V-J regio...	948	1.1e-73	1
gb	M31911	MUSIGKCRM	Mouse Ig light-chain V-J region mRN...	948	1.3e-73	1
emb	X68119	MMIGHPS4B	M.musculus gene for IgK light chain...	948	1.3e-73	1
emb	X06111	MMIGKVJ2	Mouse (hVH65-107) mRNA for immunogl...	948	1.3e-73	1
gb	M32043	MUSIGKCRT	Mouse Ig kappa-chain mRNA V-J regio...	941	5.1e-73	1
emb	X64163	HSFOG1L	H.sapiens mRNA for Fog1L kappa ligh...	939	6.3e-73	1
gb	U16689	MMU16689	Mus musculus Ig light chain leader ...	939	6.4e-73	1
gb	M17160	MUSIGCKKO	Mouse Ig kappa-chain mRNA V-region ...	939	6.7e-73	1
gb	U07211	MMU07211	Mus musculus clone 101 anti-C5a Ig ...	939	7.5e-73	1
gb	M63610	MUSIGKAVC	Mouse Ig rearranged kappa-chain (V-...	939	7.5e-73	1
gb	M20278	MUSIGKCOA	Mouse Ig active kappa chain mRNA V-...	939	7.5e-73	1
emb	X68113	MMIGHPS1B	M.musculus gene for IgK light chain...	939	7.5e-73	1
gb	M34590	MUSIGKABT	Mouse Ig kappa-chain mRNA V-J regio...	939	7.6e-73	1
emb	X05796	MMIGVK36	Mouse hybridoma 36-65 Ig L-chain re...	939	7.6e-73	1
gb	M37020	MUSIGKADS	Mouse Ig rearranged kappa-chain mRN...	939	7.6e-73	1
gb	M37021	MUSIGKADT	Mouse Ig rearranged kappa-chain mRN...	939	7.6e-73	1
emb	X53329	MMHS2H1VL	M.musculus/ H.sapiens chimeric anti...	938	2.5e-72	1
gb	M92336	MUSIGKVJE	Mouse immunoglobulin kappa light-ch...	932	2.7e-72	1
gb	M92332	MUSIGKVJC	Mouse immunoglobulin kappa light-ch...	932	2.8e-72	1
gb	M32040	MUSIGKCRQ	Mouse Ig kappa-chain mRNA V-J regio...	932	2.9e-72	1
gb	U27000	MMU27000	Mus musculus, isolate 3-7 Vk, Ig va...	930	2.9e-72	1
gb	U05217	MMU05217	Mus musculus Balb/c anti-platelet i...	930	3.6e-72	1
emb	X72463	HSIGKLV42	H.sapiens mRNA for rearranged Ig ka...	930	3.6e-72	1
gb	M85256	HUMIGKVJ	Human IgK anti-platelet integrin II...	930	4.2e-72	1
gb	S77030	S77030	Ig V kappa =H4-specific antibody li...	930	4.2e-72	1
emb	X68115	MMIGHPS2B	M.musculus gene for IgK light chain...	930	4.2e-72	1
emb	X68121	MMIGHPS5B	M.musculus gene for IgK light chain...	930	4.2e-72	1
emb	X68123	MMIGHPS6B	M.musculus gene for IgK light chain...	930	4.2e-72	1
emb	X68125	MMIGHPS7B	M.musculus gene for IgK light chain...	930	4.2e-72	1
gb	M31258	MUSIGKCRZ	Mouse active rheumatoid factor IgK ...	930	4.3e-72	1
gb	U24115	MMU24115	Mus musculus immunoglobulin F9.13.7...	927	5.2e-72	1
emb	X75854	MMIGKC1	M.musculus IgG1 mRNA for immunoglob...	787	6.0e-72	2
emb	X57639	MMMAVLC	M.musculus mRNA for monoclonal anti...	927	7.7e-72	1
gb	S60859	S60859	Ab2 kappa chain V region mAb 24 (...	927	8.1e-72	1
gb	L39092	MUSIGK527A	Mus musculus (clone 5-27) anti-fluo...	925	9.4e-72	1
gb	M31915	MUSIGKCRO	Mouse Ig light-chain V-J region mRN...	923	1.6e-71	1
gb	M29534	SYNIGHAD	Mouse heavy-chain and lambda-chain ...	921	1.6e-71	1
gb	U30238	MMU30238	Mus musculus anti-DNA antibody Ig k...	922	2.0e-71	1
dbj	D29934	MUSLCATS14	Mouse mRNA for light chain of anti-...	921	2.3e-71	1
gb	M31906	MUSIGKCRJ	Mouse Ig light-chain V-J region mRN...	921	2.4e-71	1
gb	M31910	MUSIGKCRL	Mouse Ig light-chain V-J region mRN...	921	2.4e-71	1
gb	I11959	I11959	Sequence 71 from patent US 5416202.	921	2.4e-71	1
gb	I11962	I11962	Sequence 74 from patent US 5416202.	921	2.4e-71	1

WARNING: Descriptions of 3146 database sequences were not reported due to the limiting value of parameter V = 100.

>gb|L41880|MUSIKCC Mus musculus immunoglobulin kappa chain mRNA, 5' end of cds.
Length = 390

Plus Strand HSPs:

Score = 1533 (423.6 bits), Expect = 2.4e-122, P = 2.4e-122

Identities = 313/321 (97%), Positives = 313/321 (97%), Strand = Plus / Plus

```

Query:      1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
            |||
Sbjct:     67 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 126

Query:     61 CTCACCTTGTCTGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
            |||

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Sbjct: 127 CTCACCTTGTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 186
 Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTAGGTTCTGGTGTCCCAAA 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 187 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTAGATTCTGGTGTCCCAAA 246
 Query: 181 AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 247 AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 306
 Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 307 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 366
 Query: 301 GGGACCAAGCTGGAAATAAAA 321
 ||||||||||||||||||
 Sbjct: 367 GGGACCAAGCTGGAAATAAAA 387

>gb|L48667|MUSX Mus musculus (cell line C3H/F2-15) chromosome 6 anti-DNA
 antibody light chain mRNA.
 Length = 324

Plus Strand HSPs:

Score = 1517 (419.2 bits), Expect = 6.3e-121, P = 6.3e-121
 Identities = 311/321 (96%), Positives = 311/321 (96%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 1 GANATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
 Query: 61 CTCACCTTGTGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 61 CTCACCTTGTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 120
 Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTAGGTTCTGGTGTCCCAAA 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 121 GATGGAACTTTAAACGCCTGATCTACGCCACATCCAGTTAGATTCTGGTGTCCCAAA 180
 Query: 181 AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 181 AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTGTCGTACACGTTCCGAGGG 300
 Query: 301 GGGACCAAGCTGGAAATAAAA 321
 ||||||||||||||||||
 Sbjct: 301 GGGACCAAGCTGGAAATAAAA 321

>gb|J00565|MUSIGKAC1 Mouse ig kappa active gene: vk41 v-j region.
 Length = 684

Plus Strand HSPs:

Score = 1488 (411.2 bits), Expect = 7.7e-119, P = 7.7e-119
 Identities = 308/321 (95%), Positives = 308/321 (95%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 313 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 372
 Query: 61 CTCACCTTGTGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 373 CTCACCTTGTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 432

Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAA 180
 |||
 Sbjct: 433 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAA 492

Query: 181 AGGTTTCAGTGGCAGTAGGTTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||
 Sbjct: 493 AGGTTTCAGTGGCAGTAGGTTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 552

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGGAGGG 300
 |||
 Sbjct: 553 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGA 612

Query: 301 GGGACCAAGCTGGAAATAAAA 321
 ||
 Sbjct: 613 GGCACCAAGCTGGAAATCAAA 633

>emb|V00808|MMIGK7 Part of the murine gene for kappa-immunoglobulin leader
 peptide and variable part (cell line MOPC41).
 Length = 685

Plus Strand HSPs:

Score = 1479 (408.7 bits), Expect = 4.3e-118, P = 4.3e-118
 Identities = 307/321 (95%), Positives = 307/321 (95%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||
 Sbjct: 314 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 373

Query: 61 CTCACCTTGTCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
 |||
 Sbjct: 374 CTCACCTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 433

Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAA 180
 |||
 Sbjct: 434 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAA 493

Query: 181 AGGTTTCAGTGGCAGTAGGTTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||
 Sbjct: 494 AGGTTTCAGTGGCAGTAGGTTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 553

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGGAGGG 300
 |||
 Sbjct: 554 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGA 613

Query: 301 GGGACCAAGCTGGAAATAAAA 321
 ||
 Sbjct: 614 GGCACCAAGCTGGAAATCAAA 634

>gb|103643|103643 Sequence 4 from patent US 4642334. >gb|107835|107835 Sequence
 4 from patent EP 0088994.
 Length = 324

Plus Strand HSPs:

Score = 1479 (408.7 bits), Expect = 9.1e-118, P = 9.1e-118
 Identities = 307/321 (95%), Positives = 307/321 (95%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||
 Sbjct: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60

Query: 61 CTCACCTTGTCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
 |||
 Sbjct: 61 CTCACCTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 120

Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAA 180

```

Sbjct: 121 |||GATGGA|ACTATTA|AAACGC|CTGATCTACGCC|ACATCCAGTTAGATTCTGGTGTCCCAAA 180
Query: 181 AGGTT|CAGTGG|CAGTAGGTCTGGGT|CAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
Sbjct: 181 AGGTT|CAGTGG|CAGTAGGTCTGGGT|CAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGGAGGG 300
Sbjct: 241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGA 300
Query: 301 GGGACCAAGCTGGAAATAAAA 321
Sbjct: 301 |||||GGACCAAGCTGGAAATCAAA 321

```

>gb|M59920|MUSIGKAA3 Mouse Ig germline chain mRNA V-J region, partial cds.
Length = 321

Plus Strand HSPs:

Score = 1464 (404.5 bits), Expect = 1.6e-116, P = 1.6e-116
Identities = 304/318 (95%), Positives = 304/318 (95%), Strand = Plus / Plus

```

Query: 4 ATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTC 63
Sbjct: 1 ATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTC 60
Query: 64 ACTTGT|CGGGCAAGTCAGGACATTGGTATTA|ACTTACATTGGCTTCAGCAGGAACCAGAT 123
Sbjct: 61 ACTTGT|CGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCAGAC 120
Query: 124 GGA|ACTATTA|AAACGCCTGATCTACGCC|ACATCCAGTTAGGTTCTGGTGTCCCAAAAGG 183
Sbjct: 121 GGA|ACTATTA|AAACGCCTGATCTACGCC|ACATCCAGTTAGATTCTGGTGTCCCAAAAGG 180
Query: 184 TTCAGTGGCAGTAGGTCTGGGT|CAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAA 243
Sbjct: 181 TTCAGTGGCAGTAGGTCTGGGT|CAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAA 240
Query: 244 GATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGGAGGGGGG 303
Sbjct: 241 GATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGGAGGC 300
Query: 304 ACCAAGCTGGAAATAAAA 321
Sbjct: 301 ACCAAGCTGGAAATCAAA 318

```

>gb|M36246|MUSIGLAFA Mouse Ig kappa-chain mRNA V region, partial cds, from
hybridoma H220-23.
Length = 303

Plus Strand HSPs:

Score = 1445 (399.3 bits), Expect = 6.6e-115, P = 6.6e-115
Identities = 295/303 (97%), Positives = 295/303 (97%), Strand = Plus / Plus

```

Query: 19 TCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTGGGCAAGT 78
Sbjct: 1 TCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTGGGCAAGT 60
Query: 79 CAGGACATTGGTATTA|ACTTACATTGGCTTCAGCAGGAACCAGATGGA|ACTATTAACGC 138
Sbjct: 61 CAGGACATTGGTAGAGCTTAAACTGGCTTCAGCAGGAACCAGATGGA|ACTATTAACGC 120
Query: 139 CTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAAGGTTCA|GTGGCAGTAGG 198
Sbjct: 121 CTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCAAAAGGTTCA|GTGGCAGTAGG 180

```

Query: 199 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTGTAGCCTAT 258
 |||
 Sbjct: 181 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTGTAGACTAT 240

Query: 259 TACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATA 318
 |||
 Sbjct: 241 TACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGGGGGACCAAGCTGNAATA 300

Query: 319 AAA 321
 |||
 Sbjct: 301 AAA 303

>emb|222118|MDIGKVB M.domesticus IgK variable region.
 Length = 321

Plus Strand HSPs:

Score = 1434 (396.2 bits), Expect = 5.1e-114, P = 5.1e-114
 Identities = 302/321 (94%), Positives = 302/321 (94%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||
 Sbjct: 1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60

Query: 61 CTCACCTGTGCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
 |||
 Sbjct: 61 CTCACCTGTGCGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGGAACCA 120

Query: 121 GATGGAACATTAAACGCCGTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA 180
 |||
 Sbjct: 121 GATGGAACATTAAACGCCGTGATCTACAGCACATCCACTTTAAATTCTGGTGTCCCAAAA 180

Query: 181 AGGTTTCAGTGGCAGTAGGTCCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||
 Sbjct: 181 AGGTTTCAGTGGCAGTAGGTCCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 |||
 Sbjct: 241 GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300

Query: 301 GGGACCAAGCTGGAATAAAA 321
 |||
 Sbjct: 301 GGGACCAACTGGAATAAAA 321

>gb|M64168|MUSIGKFT Mouse Ig active kappa-chain mRNA V-region.
 Length = 306

Plus Strand HSPs:

Score = 1407 (388.8 bits), Expect = 9.4e-112, P = 9.4e-112
 Identities = 291/303 (96%), Positives = 291/303 (96%), Strand = Plus / Plus

Query: 19 TCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTGCGGCAAGT 78
 |||
 Sbjct: 4 TCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTGCGGCAAGT 63

Query: 79 CAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCAGATGGAACATTAAACGC 138
 |||
 Sbjct: 64 CAGGACATTGGTAATAGCTAAACTGGCTTCAGCAGGAACCAGATGGAACATTAAACGC 123

Query: 139 CTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGG 198
 |||
 Sbjct: 124 CTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGG 183

Query: 199 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTGTAGCCTAT 258
 |||

Sbjct: 184 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAATCTGAAGATTTTGTAGTCTAT 243
 Query: 259 TACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATA 318
 |||||
 Sbjct: 244 TACTGTCTACAATATGCTAGTTATACGTACACGTTCCGAGGGGGGACCAAGTTGGAATA 303
 Query: 319 AAA 321
 |||
 Sbjct: 304 AAA 306

>emb|X02177|MMIGGVJ1 M.musculus mRNA for IgG kappa light chain (partial) Gloop
 1
 Length = 380

Plus Strand HSPs:

Score = 1362 (376.3 bits), Expect = 4.2e-108, P = 4.2e-108
 Identities = 294/321 (91%), Positives = 294/321 (91%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||
 Sbjct: 42 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 101
 Query: 61 CTCACCTGTGCGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
 |||||
 Sbjct: 102 CTCACCTGTGCGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 161
 Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGGTGCCCAAAA 180
 |||||
 Sbjct: 162 GATGGAACATTAAACGCCTGATCTACGCCGATCCACTTAGATTCTGGGTGCCCAAAA 221
 Query: 181 AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||
 Sbjct: 222 AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 281
 Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 |||||
 Sbjct: 282 GAAGATTTGTCAGACTATTACTGTCTACAATATCTTAGTTATCCGCTCACGTTCCGGTGCT 341
 Query: 301 GGGACCAAGCTGGAAATAAAA 321
 |||||
 Sbjct: 342 GGGACCAAGCTGGAGCTGAAA 362

>gb|U29617|MMU29617 Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J
 region, hybridoma 52-46A, partial cds.
 Length = 285

Plus Strand HSPs:

Score = 1357 (375.0 bits), Expect = 1.5e-107, P = 1.5e-107
 Identities = 277/284 (97%), Positives = 277/284 (97%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||
 Sbjct: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
 Query: 61 CTCACCTGTGCGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
 |||||
 Sbjct: 61 CTCACCTGTGCGGCAAGTCAGGACATTGGTAGCTTAACTGGCTTCAGCAGGAACCA 120
 Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGGTGCCCAAAA 180
 |||||
 Sbjct: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGGTGCCCAAAA 180
 Query: 181 AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||
 Sbjct: 181 AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCC 284
 |||
 Sbjct: 241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCC 284

>gb|J00566|MUSIGKVC Mouse ig kappa germline v gene: vk41. >emb|V00804|MMIGK3
 Murine kappa-immunoglobulin gene fragment including signal peptide
 and variable region.
 Length = 664

Plus Strand HSPs:

Score = 1351 (373.3 bits), Expect = 2.0e-107, P = 2.0e-107
 Identities = 279/290 (96%), Positives = 279/290 (96%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||
 Sbjct: 314 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 373

Query: 61 CTCACCTGTCTGGGCAAGTCAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCA 120
 |||
 Sbjct: 374 CTCACCTGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 433

Query: 121 GATGGAACATTTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA 180
 |||
 Sbjct: 434 GATGGAACATTTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCAAA 493

Query: 181 AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||
 Sbjct: 494 AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 553

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACAC 290
 |||
 Sbjct: 554 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCTCCAC 603

>gb|U25098|MMU25098 Mus musculus anti-Pseudomonas aeruginosa serotype IATS 06
 lipopolysaccharide O-antigen, Ig light chain variable region mRNA,
 partial cds.
 Length = 336

Plus Strand HSPs:

Score = 1353 (373.9 bits), Expect = 2.7e-107, P = 2.7e-107
 Identities = 293/321 (91%), Positives = 293/321 (91%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||
 Sbjct: 1 GAGCTCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60

Query: 61 CTCACCTGTCTGGGCAAGTCAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCA 120
 |||
 Sbjct: 61 CTCACCTGTCTGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 120

Query: 121 GATGGAACATTTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA 180
 |||
 Sbjct: 121 GATGGAACATTTAAACGCCTGATCTACGCCGATCCACTTTAGATTCTGGTGTCCCAAA 180

Query: 181 AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||
 Sbjct: 181 AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 |||
 Sbjct: 241 GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTATCCGCTGACGTTCCGGTGCT 300

Query: 301 GGGACCAAGCTGGAATAAAA 321
 |||

Sbjct: 301 GGGACCAAGCTGGAGCTGAAA 321

>emb|X02178|MMIGGVJ2 M.musculus mRNA for IgG kappa light chain (partial) Gloop
2
Length = 381

Plus Strand HSPs:

Score = 1335 (368.9 bits), Expect = 7.4e-106, P = 7.4e-106
Identities = 291/321 (90%), Positives = 291/321 (90%), Strand = Plus / Plus

```

Query:      1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
             |||
Sbjct:     43 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 102
             |||

Query:     61 CTCACCTTGTCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
             |||
Sbjct:    103 CTCACCTTGTCGGGCAAGTCAAGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 162
             |||

Query:    121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTAGGTTCTGGTGTCCCAAAA 180
             |||
Sbjct:    163 GATGGAACATTAAACGCCTGATCTACGCCCATCCACTTTAGATTCTGGTGTCCCAAAA 222
             |||

Query:    181 AGGTTCAAGTGGCAGTAGGTCTGGGTGAGTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
             |||
Sbjct:    223 AGGTTCAAGTGGCAGTAGGTCTGGGTGAGTATTCTCTCACCATCAGCAGCCTTGAGTCT 282
             |||

Query:    241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTGCGAGGG 300
             |||
Sbjct:    283 GAAGATTTTGCAGACTATTATTGTCTACAATATCTAGTTATCCGCTCACGTTGCGTGCT 342
             |||

Query:    301 GGGACCAAGCTGGAAATAAAA 321
             |||
Sbjct:    343 GGGACCAAGCTGGAGCTGAAA 363
             |||

```

>emb|X63811|MMVKMRB11 M.musculus mRNA for IgM V(k)MRB11
Length = 279

Plus Strand HSPs:

Score = 1332 (368.1 bits), Expect = 1.8e-105, P = 1.8e-105
Identities = 272/279 (97%), Positives = 272/279 (97%), Strand = Plus / Plus

```

Query:      1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
             |||
Sbjct:      1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
             |||

Query:     61 CTCACCTTGTCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
             |||
Sbjct:     61 CTCACCTTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 120
             |||

Query:    121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTAGGTTCTGGTGTCCCAAAA 180
             |||
Sbjct:    121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTAGATTCTGGTGTCCCAAAA 180
             |||

Query:    181 AGGTTCAAGTGGCAGTAGGTCTGGGTGAGTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
             |||
Sbjct:    181 AGGTTCAAGTGGCAGTAGGTCTGGGTGAGTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
             |||

Query:    241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGT 279
             |||
Sbjct:    241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGT 279
             |||

```

>gb|M12191|MUSIGKMA Mouse Ig active kappa-chain VJ2C mRNA from plasmacytoma
MOPC 173B, partial cds.
Length = 383

Plus Strand HSPs:

Score = 1326 (366.4 bits), Expect = 4.1e-105, P = 4.1e-105
 Identities = 290/321 (90%), Positives = 290/321 (90%), Strand = Plus / Plus

```

Query:   1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
          |||
Sbjct:  51 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 110

Query:   61 CTCACCTGTGCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
          |||
Sbjct:  111 CTCACATGCCGGGCAAGTCAGGACATTGATGGTTATTTAACTTGTTCAGCAGAAACCA 170

Query:   121 GATGGAACCTATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA 180
          |||
Sbjct:  171 GGTGAAACTATTAACACCTGATCTATGAAACATCCAATTTAGATTCTGGTGTCCCAAAA 230

Query:   181 AGGTTCAAGTGGCAGTAGGTCGGGTGAGTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
          |||
Sbjct:  231 AGGTTCAAGTGGCAGTAGGTCGGGTGAGTATTCTCTCATTATCGGCAGCCTTGAGTCT 290

Query:   241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTGCGAGGG 300
          |||
Sbjct:  291 GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCCTCCACGTTGCGAGGG 350

Query:   301 GGGACCAAGCTGGAAATAAAA 321
          |||
Sbjct:  351 GGGACCAAGCTGGAAATAAAA 371

```

>gb|S69053|S69053 Ig V kappa =anti-p-nitrophenyl phosphonate esterolytic
 antibody kappa chain variable region (clone CNJ206) [mice, mRNA
 Partial, 295 nt].
 Length = 295

Plus Strand HSPs:

Score = 1326 (366.4 bits), Expect = 5.3e-105, P = 5.3e-105
 Identities = 278/294 (94%), Positives = 278/294 (94%), Strand = Plus / Plus

```

Query:   21 TCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTGGGCAAGTCA 80
          |||
Sbjct:   1 TCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTGGGCAAGTCA 60

Query:   81 GGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCAGATGGAACCTATTAACGCCT 140
          |||
Sbjct:   61 GGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCAGATGGAACCTATTAACGCCT 120

Query:   141 GATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAAAGGTTCAAGTGGCAGTAGGTC 200
          |||
Sbjct:   121 GATCTACGCCGCATCCACTTTAGATTCTGGTGTCCCAAAAAGGTTCAAGTGGCAGTAGGTC 180

Query:   201 TGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGTAGCCTATTA 260
          |||
Sbjct:   181 TGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGCAGACTATTA 240

Query:   261 CTGTCTACAATATGCTAGTTCTCCGTACACGTTGCGAGGGGGGACCAAGCTGGA 314
          |||
Sbjct:   241 CTGTCTACAATATGCTAGTTCTCCGTACACGTTGCGAGGGGGGACCAAGCTGGA 294

```

>gb|U30236|MMU30236 Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J
 region, hybridoma 84.32, partial cds.
 Length = 293

Plus Strand HSPs:

Score = 1297 (358.4 bits), Expect = 1.4e-102, P = 1.4e-102

Identities = 269/281 (95%), Positives = 269/281 (95%), Strand = Plus / Plus

```

Query:   6 CCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCAC 65
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   6 CCTGATGACCCAGACTCCATCCTCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCAC 65

Query:  66 TTGTCGGGCAAGTCAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCAGATGG 125
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:  66 TTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCAGATGG 125

Query: 126 AACTATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAAGGTT 185
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 126 AACTATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCAAAAGGTT 185

Query: 186 CAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGA 245
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 186 CAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTCACCAGCAGCCTTGAGTCTGAAGA 245

Query: 246 TTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGT 286
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 246 TTTTGTAGACTATTGCTGTCTACAATATGCTAGTTCTCCGT 286

```

>gb|S55170|S55170 nitrophenyl phosphonate-specific antibody 48G7 light chain VJ
[mice, Genomic, 324 nt].
Length = 324

Plus Strand HSPs:

Score = 1290 (356.5 bits), Expect = 4.8e-102, P = 4.8e-102
Identities = 286/321 (89%), Positives = 286/321 (89%), Strand = Plus / Plus

```

Query:   1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
          || || || || || || || || || || || || || || || || || || || || ||
Sbjct:   4 GAGCTCGTGCTACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 63

Query:  61 CTCACCTGTCTGGGCAAGTCAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCA 120
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:  64 CTCACCTGTCTGGGCAAGTCAGGAAATTAATGGTTACTTAGGCTGGCTTCAGCAGAAACCA 123

Query: 121 GATGGAACATATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA 180
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 124 GATGGAACATATTAACGCCTGATCTACGCCGCATCCACTTTACATTCTGGTGTCCCAAAA 183

Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 184 AGGTTTCAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 243

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 244 GAAGATTTTGCACTATTACTGTCTGCAATATGCTAGTTATCTCGGACGTTCCGGTGA 303

Query: 301 GGGACCAAGCTGGAATAAAA 321
          || ||||| ||||| |||||
Sbjct: 304 GGCACCAAAGCTGGAATCAAA 324

```

>emb|X03382|MMIGKGA1 Mouse mRNA for GAT (HP27) anti-idiotypic Ab2 Ig (k) light
chain against public idiotopes GAT antigen = Glu(60)Ala(30)Tyr(10)
co-polymer
Length = 303

Plus Strand HSPs:

Score = 1289 (356.2 bits), Expect = 6.2e-102, P = 6.2e-102
Identities = 277/302 (91%), Positives = 277/302 (91%), Strand = Plus / Plus

```

Query:   19 TCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTCTGGGCAAGT 78
          |||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

[illegible]

>gb|J00568|MUSIGKAE mouse ig kappa unproductively rearranged gene: mopc173b v-j region. >emb|V00760|MMIG04 Mouse pseudogene for kappa-immunoglobulin.
Length = 1157

Plus Strand HSPs:

Score = 1177 (325.2 bits), Expect = 7.2e-101, Sum P(2) = 7.2e-101
Identities = 257/284 (90%), Positives = 257/284 (90%), Strand = Plus / Plus

```

Query:      1  GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT  60
             |||||||
Sbjct:     547 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT  606
             |||||||

Query:      61  CTCACCTGTCTGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCA  120
             |||||||
Sbjct:     607 CTCACCTGCCGGGCAAGTCAGGACATTGATGGTTATTTAAACTGTGTTTCAGCAGAAACCA  666
             |||||||

Query:      121 GATGGAACATTTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA  180
             |||||||
Sbjct:     667 GGTGAAACATTTAAACACCTGATCTATGAACATCCAATTTAGATTCTGGTGTCCCCAAA  726
             |||||||

Query:      181 AGGTTCAAGTGGCAGTAGGTCGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT  240
             |||||||
Sbjct:     727 AGGTTCAAGTGGCAGTAGGTCGGGTCAGATTATTCTCTCATTTATCGGCAGCCTTGAGTCT  786
             |||||||

Query:      241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCC  284
             |||||||
Sbjct:     787 GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCC  830
             |||||||

```

Score = 170 (47.0 bits), Expect = 7.2e-101, Sum P(2) = 7.2e-101
Identities = 34/34 (100%), Positives = 34/34 (100%), Strand = Plus / Plus

Query: 288 CACGTTCTGGAGGGGGGACCAAGCTGGAATAAAA 321
 |||||
 Sbjct: 833 CACGTTCTGGAGGGGGGACCAAGCTGGAATAAAA 866

```
>gb|U19320|MMU19320 Mus musculus immunoglobulin kappa light chain variable
      region mRNA, clone MRL2-117, partial cds.
      Length = 293
```

Plus Strand HSPs:

Score = 1276 (352.6 bits), Expect = 7.7e-101, P = 7.7e-101
Identities = 272/293 (92%), Positives = 272/293 (92%), Strand = Plus / Plus

```

Query:   25 TCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTCGGGCAAGTCAGGAC 84
          |||
Sbjct:   1  TCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCGGGCAAGTCAGGAA 60

Query:   85 ATTGGTATTAACCTACATTGGCTTCAGCAGGAACCAGATGGAACATTAAACGCCTGATC 144
          |||
Sbjct:   61 ATTAGTGGTTACTTAAGCTGGCTTCAGCAAAAACCAGATGGAACATTAAACGCCTGATC 120

Query:   145 TACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGG 204
          |||
Sbjct:   121 TACGCCGCATCCACTTTAGATTCTGGTGTCCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGG 180

Query:   205 TCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGT 264
          |||
Sbjct:   181 TCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGCAGACTATTACTGT 240

Query:   265 CTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGAAAT 317
          |||
Sbjct:   241 CTACAATATGCTAGTTATCCGTATACGTTTCGGATCGGGGACCAAGCTGGAAAT 293

```

>emb[X03383]MMIGKA2 Mouse mRNA for GAT (HP22) anti-idiotypic Ab2 Ig (k) light chain against public idiotopes GAT antigen = Glu(60)Ala(30)Tyr(10) co-polymer
Length = 297

Plus Strand HSPs:

Score = 1270 (350.9 bits), Expect = 2.4e-100, P = 2.4e-100
Identities = 272/297 (91%), Positives = 272/297 (91%), Strand = Plus / Plus

```

Query:   25 TCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTCGGGCAAGTCAGGAC 84
          |||
Sbjct:   1  TCTTCCTTATCTGCCNCTCTGGGAGAAAGAGNCNGTCTCACTTGTCGGGCAAGTCAGGAT 60

Query:   85 ATTGGTATTAACCTACATTGGCTTCAGCAGGAACCAGATGGAACATTAAACGCCTGATC 144
          |||
Sbjct:   61 ATTAGTGGTTACTTAAACTGGCTTCAGCGGAAACTAGATGGAACATTAAACGCCTGATC 120

Query:   145 TACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGG 204
          |||
Sbjct:   121 TACAGCACATCCACTTTAGATTCTGGTGTCCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGG 180

Query:   205 TCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGT 264
          |||
Sbjct:   181 TTAGATTATTCTCTCACCATCAGCAGCCTAGAGTCTGAAGATTTTGCAGACTATTNCTGT 240

Query:   265 CTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA 321
          |||
Sbjct:   241 CTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGGGGGACCAAGCNGGAAATAAAA 297

```

>gb[U21066]MMU21066 Mus musculus immunoglobulin kappa chain V-J regions mRNA, clone MRL3-7, partial cds.
Length = 273

Plus Strand HSPs:

Score = 1121 (309.8 bits), Expect = 1.3e-98, Sum P(2) = 1.3e-98
Identities = 233/244 (95%), Positives = 233/244 (95%), Strand = Plus / Plus

```

Query:   67 TGTCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCAGATGGA 126
          |||
Sbjct:   30 TGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCAGATGGA 89

Query:   127 ACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAAAGGTTTC 186
          |||
Sbjct:   90 ACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGGTTTC 149

```

Query: 187 AGTGGCAGTAGGCTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGAT 246
 |||||
 Sbjct: 150 AGTGGCAGTAGGCTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGAT 209

Query: 247 TTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGGGGGACC 306
 |||||
 Sbjct: 210 TTTGTAGACTATTACTGTCTACAATATGCTTTTCTCCGTATACGTTCCGATCGGGGACC 269

Query: 307 AAGC 310
 ||||
 Sbjct: 270 AAGC 273

Score = 141 (39.0 bits), Expect = 1.3e-98, Sum P(2) = 1.3e-98
 Identities = 29/30 (96%), Positives = 29/30 (96%), Strand = Plus / Plus

Query: 37 GCCTCTCTGGGACAAAGAGTCAGTCTCACT 66
 |||||
 Sbjct: 1 GCCTCTCTGGGAGAAAGAGTCAGTCTCACT 30

>gb|L22571|MUSIGKAF2 Mouse IgK chain mRNA V-region.
 Length = 270

Plus Strand HSPs:

Score = 557 (153.9 bits), Expect = 1.5e-97, Sum P(5) = 1.5e-97
 Identities = 117/124 (94%), Positives = 117/124 (94%), Strand = Plus / Plus

Query: 177 CAAAAGGTTCACTGGCAGTAGGCTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGA 236
 |||||
 Sbjct: 147 CAAAAGGTTCACTGGCAGTAGGCTCTGGGTCAGATCATTTCTCACCATCACCAGCCTTGA 206

Query: 237 GTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCG 296
 |||||
 Sbjct: 207 GTCTGAAGATTTTGTAGACTATTACTGTCTTCAATATGTTAGTTCTCCGTACACGTTCCG 266

Query: 297 AGGG 300
 ||||
 Sbjct: 267 AGGG 270

Score = 398 (110.0 bits), Expect = 1.5e-97, Sum P(5) = 1.5e-97
 Identities = 86/94 (91%), Positives = 86/94 (91%), Strand = Plus / Plus

Query: 25 TCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTCCGGCAAGTCAGGAC 84
 |||||
 Sbjct: 1 TCCTCCTTATCTGCCTCTCTGGGAGAGAGAGTCAGTCTCACTTGTCCGGCAAGTCAGGAC 60

Query: 85 ATTGGTATTAACCTACATTGGCTTCAAGAGAAC 118
 |||||
 Sbjct: 61 ATTGGTAATAGCTTAACTGGCTTCAACAGGAGC 94

Score = 111 (30.7 bits), Expect = 1.5e-97, Sum P(5) = 1.5e-97
 Identities = 23/24 (95%), Positives = 23/24 (95%), Strand = Plus / Plus

Query: 132 TAAACGCCTGATCTACGCCACATC 155
 |||||
 Sbjct: 106 TTAACGCCTGATCTACGCCACATC 129

Score = 91 (25.1 bits), Expect = 1.5e-97, Sum P(5) = 1.5e-97
 Identities = 19/20 (95%), Positives = 19/20 (95%), Strand = Plus / Plus

Query: 156 CAGTTTAGGTTCTGGGTGTC 175
 |||||
 Sbjct: 129 CAGTTTAGATTCTGGGTGTC 148

Score = 82 (22.7 bits), Expect = 1.5e-97, Sum P(5) = 1.5e-97
 Identities = 18/20 (90%), Positives = 18/20 (90%), Strand = Plus / Plus

Query: 115 GAACCAGATGGAACATTAA 134
 |||||
 Sbjct: 90 GGAGCAGATGGAACATTAA 109

>gb|M20832|MUSIGKLN Mouse IgMk rearranged kappa light-chain mRNA variable
 region (V-J-kappa) anti-DNA autoantibody.
 Length = 413

Plus Strand HSPs:

Score = 1200 (331.6 bits), Expect = 1.2e-94, P = 1.2e-94
 Identities = 276/321 (85%), Positives = 276/321 (85%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||
 Sbjct: 93 GACATCCAGATGATTAGTCTCCATCGTCCATGTTGGCTCTCTGGGAGACAGAGTCAGT 152
 Query: 61 CTCACCTGTGCGGGCAAGTCAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCA 120
 |||||
 Sbjct: 153 CTCTCTTGCCGGGCTAGTCAGGGCATTAGAGGTAATTTAGACTGGTATCAGCAGAAACCA 212
 Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA 180
 |||||
 Sbjct: 213 GGTGGAACATTAAACTCCTGATCTACTCCACATCCAATTTAAATTCTGGTGTCCCATCA 272
 Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||
 Sbjct: 273 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTAGAGTCT 332
 Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 |||||
 Sbjct: 333 GAAGATTTTGCAGACTATTACTGTCTACAGCGTAATGCGTATCCGTACACGTTCCGAGGG 392
 Query: 301 GGGACCAAGCTGGAAATAAAA 321
 |||||
 Sbjct: 393 GGGACCAAGCTGGAAATAAAA 413

>gb|U20061|MMU20061 Mus musculus anti-DNA antibody immunoglobulin kappa chain
 mRNA, clone A6.1Vkappa, partial cds.
 Length = 324

Plus Strand HSPs:

Score = 1191 (329.1 bits), Expect = 8.2e-94, P = 8.2e-94
 Identities = 275/321 (85%), Positives = 275/321 (85%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||
 Sbjct: 1 GACATCCAGATGATTAGTCTCCATCGTCCATGTTGCCTCTCTGGGAGACAGAGTCAGT 60
 Query: 61 CTCACCTGTGCGGGCAAGTCAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCA 120
 |||||
 Sbjct: 61 CTCTCTTGCCGGGCTAGTCAGGGCATTAGAGGTAATTTAGACTGGTATCAGCAGAAACCA 120
 Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA 180
 |||||
 Sbjct: 121 GGTGGAACATTAAACTCCTGATCTACTCCACATCCAATTTAAATTCTGGTGTCCCATCA 180
 Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||
 Sbjct: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTAGAGTCT 240
 Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 |||||
 Sbjct: 241 GAAGATTTTGCAGACTATTACTGTCTACAGCGTAATGCGTATCCGTCTCACGTTCCGAGGG 300
 Query: 301 GGGACCAAGCTGGAAATAAAA 321

Sbjct: 301 GGGACCAAGCTGGAAATAAAA 321

>gb|M33559|MUSIGKABE Mouse Ig rearranged kappa-chain mRNA V-J2-region,
hybridoma A6.1, partial cds.
Length = 321

Plus Strand HSPs:

Score = 1191 (329.1 bits), Expect = 8.3e-94, P = 8.3e-94
Identities = 275/321 (85%), Positives = 275/321 (85%), Strand = Plus / Plus

```

Query:      1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
             |||
Sbjct:      1 GACATCCAGATGATTAGTCAGTCTCCATCGTCCATGTTTGCCTCTCTGGGAGACAGAGTCAGT 60
             |||

Query:     61 CTCACCTTGTCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
             |||
Sbjct:     61 CTCCTCTTGTCGGGCTAGTCAGGGCATTAGAGGTAATTTAGACTGGTATCAGCAGAAACCA 120
             |||

Query:    121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA 180
             |||
Sbjct:    121 GGTGGAACATTAAACCTCTGATCTACTCCACATCCAATTTAAATTCTGGTGTCCCATCA 180
             |||

Query:    181 AGGTTTCAGTGGCAGTAGGTCTGGGTCTAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
             |||
Sbjct:    181 AGGTTTCAGTGGCAGTAGGTCTGGGTCTAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
             |||

Query:    241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGG 300
             |||
Sbjct:    241 GAAGATTTTGCAGACTATTACTGTCTACAGCGTAATGCGTATCTCTCACGTTTCGGAGGG 300
             |||

Query:    301 GGGACCAAGCTGGAAATAAAA 321
             |||
Sbjct:    301 GGGACCAAGCTGGAAATAAAA 321
             |||

```

>gb|K00880|MUSIGKVE mouse ig kappa germline v gene: mopc173b.
Length = 675

Plus Strand HSPs:

Score = 1180 (326.1 bits), Expect = 1.3e-91, P = 1.3e-91
Identities = 260/290 (89%), Positives = 260/290 (89%), Strand = Plus / Plus

```

Query:      1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
             |||
Sbjct:    325 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 384
             |||

Query:     61 CTCACCTTGTCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
             |||
Sbjct:    385 CTCACCTTGCCGGGCAAGTCAGGACATTATGGTTATTTAAACTTGTTCAGCAGAAACCA 444
             |||

Query:    121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA 180
             |||
Sbjct:    445 GGTGAAACTATTAAACACCTGATCTATGAAACATCCAATTTAGATTCTGGTGTCCCAAAA 504
             |||

Query:    181 AGGTTTCAGTGGCAGTAGGTCTGGGTCTAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
             |||
Sbjct:    505 AGGTTTCAGTGGCAGTAGGTCTGGGTCTAGATTATTCTCTCATTATCGGCAGCCTTGAGTCT 564
             |||

Query:    241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACAC 290
             |||
Sbjct:    565 GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCCTCCAC 614
             |||

```

>gb|U16180|MMU16180 Mus musculus anti-cardiolipin antibody CAL Ig light chain
mRNA, partial cds.

Length = 321

Plus Strand HSPs:

Score = 1137 (314.2 bits), Expect = 2.6e-89, P = 2.6e-89
 Identities = 269/321 (83%), Positives = 269/321 (83%), Strand = Plus / Plus

```

Query:   1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:   1 GACATCCAGATGATTAGTCTCCATCGTCCATGTTTGCCTTCTGGGAGACAGATCAGT 60

Query:  61 CTCACCTTGTCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  61 CCTTCTTGTCGGGCTAGTCAGGGCAAAGAGGTAATTTAGACTGGTATCAGCAGAAACCA 120

Query:  121 GATGGAACCTATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA 180
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  121 GGTGGAACCTATTAACCTCTTGATCTACTCCACATCCAATTTAAATCTGGTGTCCCATCA 180

Query:  181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTAGAGTCT 240
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  181 AGGTTTCAGTGGCAGTGGGTCGGGTCAGATTATTCTCTCACCATCAGCAGCCTTAGAGTCT 240

Query:  241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  241 GAAGATTTTGCAGACTATTACTGTCTACAGCGTAATGCCTTCCGTACACGTTCCGAGGG 300

Query:  301 GGGACCAAGCTGGAAATAAAA 321
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  301 GGGACCAAGCTGGAAATAAAA 321

```

>emb|x03384|MMIGKGA3 Mouse mRNA for GAT (HP29) anti-idiotypic Ab2 Ig (k) light
 chain against public idiotopes GAT antigen = Glu(60)Ala(30)Tyr(10)
 co-polymer
 Length = 276

Plus Strand HSPs:

Score = 1137 (314.2 bits), Expect = 3.0e-89, P = 3.0e-89
 Identities = 249/276 (90%), Positives = 249/276 (90%), Strand = Plus / Plus

```

Query:   46 GGACAAAGAGTCAGTCTCACTTGTGGGCAAGTCAGGACATTGGTATTAACCTACATTGG 105
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:   1 GGAGAAAGAGAAAGTCTCACTTGTGGGCAAGTCAGGATATTAGTGTTTACTTAACTGG 60

Query:  106 CTTCAGCAGGAACCAGATGGAACCTATTAACGCCTGATCTACGCCACATCCAGTTTAGGT 165
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:   61 CTTCAGCAGAACTAGATGGAACCTATTAACGCCTGATTTACAGCACATCCATTTAGAT 120

Query:  166 TCTGGTGTCCCAAAAGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATC 225
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  121 TCTGGTGTCCCAAAAGGTTCAAGTGGCAGTAGGTCTGGAACAGATTATTCTCTCACCATC 180

Query:  226 AGCAGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCG 285
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  181 AACAGCCTAGAGTCTGAAGATTTTGCAGACTATTCTGTCTCCAATATGCTAGTTCTCCG 240

Query:  286 TACACGTTCCGAGGGGGGACCAAGCTGGAAATAAAA 321
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  241 TTCACATTCGGAGGGGGGACCAAGCTGGAAATAAAA 276

```

>gb|U19327|MMU19327 Mus musculus immunoglobulin kappa light chain variable
 region mRNA, clone MRL2-17, partial cds.
 Length = 261

Plus Strand HSPs:

```

Query:      1  GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT  60
              |||
Sbjct:      1  GATATCCAGATGACACAGACTACATCCTCCTGTCTGCCTCTCTGGGAGACAGAGTCACC  60
              |||
Query:     61  CTCACCTTGTCGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCA  120

```

```
Score = 1011 (279.4 bits), Expect = 7.3e-79, P = 7.3e-79  
Identities = 255/321 (79%), Positives = 255/321 (79%), Strand = Plus / Plus
```

Query: 1 GACATCCAGATGACCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAGAGTCAGT 60
f ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 19 GATATCCAGATGACACAGACTACATCCTCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 78

Query: 61 CTCACTTGTCGGGCCAAGTCAGGACATTGGTTAACTTACATTGGCTTCAGCAGGAACCA 120
 ||| ||||| | | | | | | | | | | | | | | | | | | | | |
Sbjct: 79 ATCAGTTGCAGGGCAAAGTCAGGACATTAGCAATTATTTAAACTGGTATCAGCAGAAACCA 138

Query: 121 GATGGAAC TATTA ACGC CTGATCTACGCC ACATCC AGTTTAG GTTCT GG TGTC CCCC AAA 180

```

Sbjct: 139 GATGGAAGCTGTTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 198
Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
Sbjct: 199 AGGTTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAA 258
Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTGCGAGGG 300
Sbjct: 259 GAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTACACGTTGCGAGGG 318
Query: 301 GGGACCAAGCTGGAAATAAAA 321
Sbjct: 319 GGGACCAAGCTGGAAATAAAA 339

```

```
>gb|M63611|MUSIGKAVD Mouse Ig rearranged kappa-chain (V-I dCR J2) gene V10-J
region, hybridoma KL2.29, partial cds. >gb|M63612|MUSIGKAVE Mouse
Ig rearranged kappa-chain (V-I dCR J2) gene V10-J region, hybridoma
KL2.33, partial cds. >gb|M63613|MUSIGKAVF Mouse Ig rearranged
kappa-chain (V-I dCR J2) gene V10-J region, hybridoma KL3.8, partial
cds. >emb|X55044|MMIGKL229 M.musculus gene for immunoglobulin kappa
light chain variable region (KL2.29) >emb|X55045|MMIGKL233
M.musculus gene for immunoglobulin kappa light chain variable
region (KL2.33) >emb|X55046|MMIGKL38 M.musculus gene for
immunoglobulin kappa light chain variable region (KL3.8)
Length = 324
```

Plus Strand HSPs:

Score = 1011 (279.4 bits), Expect = 7.7e-79, P = 7.7e-79
Identities = 255/321 (79%), Positives = 255/321 (79%), Strand = Plus / Plus

[illegible]

>gb|M63609|MUSIGKAVB Mouse Ig rearranged kappa-chain (V-I dCR J1) gene V10-J region, hybridoma KL2.21, partial cds. >emb|X55042|MMIGKL221 M.musculus gene for immunoglobulin kappa light chain variable region (KL2.21)
Length = 321

Plus Strand HSPs:

Score = 832 (229.9 bits), Expect = 2.6e-78, Sum P(2) = 2.6e-78
Identities = 212/269 (78%), Positives = 212/269 (78%), Strand = Plus / Plus

[illegible]

Score = 184 (50.8 bits), Expect = 2.6e-78, Sum P(2) = 2.6e-78
Identities = 56/80 (70%), Positives = 56/80 (70%), Strand = Plus / Plus

```

Query: 242 AAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGGAGGGG 301
      |||||
Sbjct: 239 AAGAAGATATTGCCACTTACTTTGCCAACAGGGTAATACGCTGTGGACGTTCCGGTGGAG 298

Query: 302 GGACCAAGCTGGAAATAAA 321
      |||||
Sbjct: 299 GCACCAAGCTGGAAATCAA 318

```

>gb|U20820|MMU20820 Mus musculus Ig Fab F9.13.7 light chain mRNA, partial cds.
Length = 330

Plus Strand HSPs:

Score = 993 (274.4 bits), Expect = 2.4e-77, P = 2.4e-77
Identities = 253/321 (78%), Positives = 253/321 (78%), Strand = Plus / Plus

[illegible]

```
>gb|M36261|MUSIGLAPP Mouse Ig kappa-chain mRNA V region, partial cds, from
    hybridoma L2-10C1.
    Length = 321
```

Score = 993 (274.4 bits), Expect = 2.5e-77, P = 2.5e-77
Identities = 253/321 (78%), Positives = 253/321 (78%), Strand = Plus / Plus

```

Query:      1  GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT  60
             |||
Sbjct:      1  GATATCCAGATGACACAGACTACATCCTCCCTGCTGCCTCTCTGGGAGACAGAGTCACC  60

Query:     61  CTCACCTGTGCGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA  120
             |||
Sbjct:     61  ATCAGTTGCAGTGCAAGTCAGGGCATTAGCAATTATTTAAACTGGTATCAGCAGAAACCA  120

Query:    121  GATGGAACATTATAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA  180
             |||
Sbjct:    121  GATGGAACGTATAAAGCTGATCTATTACACATCAAGTTTAACTCAGGAGTCCCATCA  180

Query:    181  AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT  240
             |||
Sbjct:    181  AGGTTCAAGTGGCAGTAGGTCTGGGACAGATTATTCTCTCACCATCAGCAACCTGGAACCT  240

Query:    241  GAAGATTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTGCGAGGG  300
             |||
Sbjct:    241  GAAGATATTGCCACTTACTATTGTCAGCAGTATAGTAAGCTTCCGTGGACGTTGCGTGA  300

Query:     301  GGGACCAAGCTGGAAATAAAA  321
             ||
Sbjct:     301  GGCACCAAGCTGGAAATCAAA  321

```

>gb|M63614|MUSIGKAVG Mouse Ig rearranged kappa-chain (V-IdCR J1) gene V10-J region, hybridoma KL4A1, partial cds. >gb|M63616|MUSIGKAVI Mouse Ig rearranged kappa-chain (V-IdCR J1) gene V10-J region, hybridoma KL4C8, partial cds. >emb|X55047|MMIGKL4A1 M.musculus gene for immunoglobulin kappa light chain variable region (KL4A1)
Length = 321

Score = 832 (229.9 bits), Expect = 8.0e-77, Sum P(2) = 8.0e-77
Identities = 212/269 (78%), Positives = 212/269 (78%), Strand = Plus / Plus

```

Query:      1  GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT  60
             |||||
Sbjct:      1  GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC  60

Query:     61  CTCACTTGTCTGGGCAAGTCAGGACATTGGTATTAACATTACATTGGCTTCAGCAGGAACCA  120
             |||||
Sbjct:     61  ATCAGTTGCAGGGCAAGTCAGGACATTAGCAATTATTTAACTGGTATCAGCAGAAACCA  120

Query:    121  GATGGAACATTAATAACGCCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA  180
             |||||
Sbjct:    121  GATGGAACGTGTTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA  180

Query:    181  AGGTTTCAGTGGCAGTAGGTCGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT  240
             |||||
Sbjct:    181  AGGTTTCAGTGGCAGTGGGCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAA  240

Query:    241  GAAGATTTTGTAGCCTATTACTGTCTACA  269
             |||||
Sbjct:    241  GAAGATATTGCCACTTACTTTGCCAACA  269

```

Score = 166 (45.9 bits), Expect = 8.0e-77, Sum P(2) = 8.0e-77
Identities = 54/80 (67%), Positives = 54/80 (67%), Strand = Plus / Plus

Query: 242 AAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGGG 301
||| | ||| |||| | |||| |||| |||| ||||
Sbjct: 239 AAGAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCGGACGTTTCGGTGAAG 298

Query: 302 GGACCAAGCTGGAAATAAAA 321
 |||||
 Sbjct: 299 GCACCAAGCTGGAAATCAA 318

>emb|x70090|MMNL4H10 M.musculus NL4H10 mRNA for immunoglobulin light chain,
 variable region
 Length = 321

Plus Strand HSPs:

Score = 986 (272.4 bits), Expect = 9.4e-77, P = 9.4e-77
 Identities = 252/321 (78%), Positives = 252/321 (78%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||
 Sbjct: 1 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 60

Query: 61 CTCACCTGTCTGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
 |||||
 Sbjct: 61 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAATTATTTACACTGGTATCAGCAGAAACAA 120

Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA 180
 |||||
 Sbjct: 121 GATGGAACGTAAACTNCTGATCTACTACACTAAGATTACATTCAGGAGTCCCATCA 180

Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||
 Sbjct: 181 AGGTTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAA 240

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTGGGAGGG 300
 |||||
 Sbjct: 241 GAAGATATTGCCACTTACTTTTGCCAACAGGCTAATACGCTTCCGTACACGTTGGGAGGG 300

Query: 301 GGGACCAAGCTGGAAATAAAA 321
 |||||
 Sbjct: 301 GGGACCAAGCTGGAAATAAA 321

>gb|M60020|MUSIGKAAAM Mouse Ig kappa chain mRNA V-J region, 5' end.
 Length = 395

Plus Strand HSPs:

Score = 984 (271.9 bits), Expect = 1.1e-76, P = 1.1e-76
 Identities = 252/321 (78%), Positives = 252/321 (78%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||
 Sbjct: 72 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 131

Query: 61 CTCACCTGTCTGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
 |||||
 Sbjct: 132 ATCAGTTGCAGTGCAAGTCAGGGCATTAGTAATTATTAACTGGTATCAGCAGAAACCA 191

Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA 180
 |||||
 Sbjct: 192 GATGGAACGTAAACTCCTGATCTATTACACATCAAGATTACACTCAGGAGTCCCATCA 251

Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||
 Sbjct: 252 AGGTTTCAGTGGCAGTGGGTCTGGGACAGATTATTCTCTCACCATCAGCAACCTGGAACCT 311

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTGGGAGGG 300
 |||||
 Sbjct: 312 GAAGATATTGCCACTTATTTTGTGACAGATAGTAAGTTCCATTACGTTGGGCTCG 371

Query: 301 GGGACCAAGCTGGAAATAAAA 321
 |||||

>gb|S50261|S50261 Ig VL=anti-CD4 mAb M-T151 variable region light chain (J2,
chimeric antibody) [mice, hybridoma cells, mRNA Partial, 381 nt].
Length = 381

Plus Strand HSPs:

Score = 984 (271.9 bits), Expect = 1.2e-76, P = 1.2e-76
Identities = 252/321 (78%), Positives = 252/321 (78%), Strand = Plus / Plus

[illegible]

>gb|M84440|MUSIGLCC Mouse rearranged light chain variable region gene sequence.
Length = 360

Plus Strand HSPs:

Score = 984 (271.9 bits), Expect = 1.2e-76, P = 1.2e-76
Identities = 252/321 (78%), Positives = 252/321 (78%), Strand = Plus / Plus

```
Query:      1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAGAGTCAGT   60
            || | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     10 GATGTCA TGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC   69

Query:     61 CTCAC TTGT CGGGCAA GT CAGGACATTGG TATTA AACTT ACATT GGCTT CAGCAGGA ACCA    120
            ||| ||| | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     70 ATCAGTTGCAGTGCAAGTCAGGGCATTAGCAATTA TTAA ACTGGTATCAGCAGAAA CCA    129

Query:    121 GATGGA ACTAT TA AACG CCTGAT CTACGCC ACATCC AGTT TAGGTT CTGGTGT CCCCAA A    180
            ||||| ||| | | | | | | | | | | | | | | | | | | | | |
Sbjct:    130 GATGGA ACTGT TAA ACTC CTGATCT ATTACAC ATCAAGTT TACACT CAGGAGT CCCAT CA   189

Query:    181 AGGTTCA GTGGCAG TAGGTCT GGGTCAG ATTAT TCCTC ACCATC AGCAGC CTTGAGT CT   240
            || | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    190 AGGTTCA GTGGCAG TGGGTCT GGGACAG ATTAT TCCTC ACCATC AGCAAC CTGGAAC CT   249

Query:    241 GAAGAT TTTGT AGCCTAT TACTGT CTACA ATATG CTAGT TCTCCGT ACACG TTCGGAG GG   300
            || | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    250 GAAGAT GTTGCCA CTATTAT TTGTG CAGAAT ATAGT AAGGTT CCGTGG ACGTT CCGT GGA   309

Query:    301 GGGACCA AGCTG GAAATA AAAA        321
            || | | | | | | | | | | | | | | | | |
Sbjct:    310 GGCACCA AGCTG GAAAT CAAA       330
```

>emb|x65095|MMIGLC151 M.musculus mRNA for IG light chain VJ region (M-T151)
Length = 324

Plus Strand HSPs:

Score = 984 (271.9 bits), Expect = 1.4e-76, P = 1.4e-76
Identities = 252/321 (78%), Positives = 252/321 (78%), Strand = Plus / Plus

```

Query:   1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   1 GATATCCAGATGACACAGACTATATCCTCCCTCTCTGCCTCTCTGGGAGACAGAGTCACC 60

Query:   61 CTCAC TTGTGCGGCAAGTCAGGACATTGGTATTAAC TTACATTGGCTTCAGCAGGAACCA 120
          ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   61 ATCAG TTGCAGGCAAGTCAGGACATTAACAATTATTTAAGCTGGTATCAGCAGAAACCA 120

Query:   121 GATGGAAC TATTAACGCCTGATCTACGCCACATCCAGTTAGGTTCTGGTGTCCCAAA 180
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   121 GATGGAAC GTTAACTCCTGATCTACTACACATCAAGATTACATT CAGGAGTCCCATCA 180

Query:   181 AGGTT CAGTGGCAGTAGGCTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   181 AGGTT CAGTGGCAGTGGGCTCTGGAACAGATTATTCTCTCACCATTACCAACCTGGAGCAA 240

Query:   241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   241 GAAGAT GTTGCCACTTACTTTTGCCAACAGGGTAATACGTTCCGTACACGTTCCGAGGG 300

Query:   301 GGGACCAAGCTGGAAATAAAA 321
          ||||| ||||| ||||| |||||
Sbjct:   301 GGGACCAAGCTGGAAATAAAA 321

```

>gb|S76654|S76654 Ig VL=F30C7 light chain variable region [mice, hybridoma,
mRNA Partial, 321 nt].
Length = 321

Plus Strand HSPs:

Score = 984 (271.9 bits), Expect = 1.4e-76, P = 1.4e-76
Identities = 252/321 (78%), Positives = 252/321 (78%), Strand = Plus / Plus

```

Query:   1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   1 GATATT CAGATGACACAGTCTTCATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 60

Query:   61 CTCAC TTGTGCGGCAAGTCAGGACATTGGTATTAAC TTACATTGGCTTCAGCAGGAACCA 120
          ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   61 ATCAG TTGCAGGGCAAGTCAGGATATTAGCAATTATTTAACTGGTATCAGCAGAAACCA 120

Query:   121 GATGGAAC TATTAACGCCTGATCTACGCCACATCCAGTTAGGTTCTGGTGTCCCAAA 180
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   121 GATGGAAC GTTAACTCCTGATCTACTACACATCAAGATTACACT CAGGAGTCCCATCA 180

Query:   181 AGGTT CAGTGGCAGTAGGCTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   181 AGGTT CAGTGGCAGTGGGCTCTGGGACAGATTATTCTCTCACCATCAGCAACCTGGAACT 240

Query:   241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   241 GAAGAT ATTGCCACTTACTATTGT CAGCAGTATAGTAACCTCCGCTCAGGTTCCGGTGCT 300

Query:   301 GGGACCAAGCTGGAAATAAAA 321
          ||||| ||||| ||||| |||||
Sbjct:   301 GGGACCAAGCTGGAGCTGAAA 321

```

>gb|M36242|MUSIGLAEW Mouse Ig kappa-chain mRNA V region, partial cds, from

Plus Strand HSPs:

```
>emb|X85995|HSDELIGVJ H.sapiens mRNA for immunoglobulin kappa light chain
variable region (patient DEL)
Length = 388
```

Plus Strand HSPs:

```

Query:      1  GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT  60
             |||||||||||||||||||||||||||||||||||||||||||
Sbjct:     67  GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC  126

Query:     61  CTCACCTGTGCGGCAAGTCAGGACATTGGTATTAACATTACATTGGCTTCAGCAGGAACCA  120
             |||||||  |||||||||||||||||||  |||  |||  |||  |||  |||  |||
Sbjct:    127  ATCACTTGCCAGGCGAGTCAGGACATTAGTAATATTTAAATTGGTATCAGCAGAAACCA  186

Query:    121  GATGGAACATATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA  180
             |  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Sbjct:    187  GGGAAAGCCCTAAGCTCCTGATCCACGCTGCATCCAGTTTGGAAACAGGGGTCCCATCA  246

Query:    181  AGGTTCA GTGGCAGTAGGTCTGGGT CAGATTAT TCTCTCACCATCAGCAGCCTTGAGTCT  240
             |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Sbjct:    247  AGGTTCA GTGGAAGTGGGTCTGGGACAGATTTTCTTTCAACCATCAGCAGCCTACAGCCT  306

Query:    241  GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGG  300
             |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Sbjct:    307  GAAGATCTTGCAACATATTACTGCCAACAGTATGATAATCTCCGCTCACTTTCGGCGGG  366

Query:    301  GGGACCAAGCTGGAAATAAAA 321
             |||  |||  |||  |||  |||
Sbjct:    367  GGGACCAAGGTGGAGATCAAA 387

```

```
>gb|M84434|MUSIGLAC Mouse rearranged light chain variable region gene sequence.
      Length = 360
```

Plus Strand HSPs:

Score = 975 (269.4 bits), Expect = 6.9e-76, P = 6.9e-76
 Identities = 251/321 (78%), Positives = 251/321 (78%), Strand = Plus / Plus

```

Query:   1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
          || || || || || || || || || || || || || || || || || || || || ||
Sbjct:  10 GATGTCATGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 69

Query:   61 CTCACTTGTCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
          || || || || || || || || || || || || || || || || || || || || ||
Sbjct:  70 ATCAGTTGCAGTGAAGTCAGGGCATTAGCAATTATTTAACTGGTATCAGCATAAACCA 129

Query:  121 GATGGAACCTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA 180
          || || || || || || || || || || || || || || || || || || || || ||
Sbjct:  130 GATGGAACCTGTTAACTCCTGATCTATTACACATCAAGTTTACACTCAGGAGTCCCATCA 189

Query:  181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
          || || || || || || || || || || || || || || || || || || || || ||
Sbjct:  190 AGGTTTCAGTGGCAGTGGGTCTGGGACAGATTATTCTCTCACCATCAGCAACCTGGAACCT 249

Query:  241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGG 300
          || || || || || || || || || || || || || || || || || || || || ||
Sbjct:  250 GAAGATGTTGCCACTTATTATTGTCTAGCAATATAGTAAGGTTCCGTGGACGTTTCGGTGGA 309

Query:  301 GGGACCAAGCTGGAATAAAA 321
          || || || || || || || || || || || || || || || || || || || || ||
Sbjct:  310 GGCACCAAGCTGGAATCAAA 330
  
```

WARNING: HSPs involving 3196 database sequences were not reported due to the limiting value of parameter B = 50.

Parameters:

V=100
 B=50
 H=1
 -qtype
 E=10

-ctxfactor=2.00

Query	Strand	MatID	Matrix name	----- Lambda	As Used K	----- H	----- Lambda	Computed K	----- H
+1	0	+5,-4	0.192	0.173	0.357	same	same	same	
-1	0	+5,-4	0.192	0.173	0.357	same	same	same	

Query	Strand	MatID	Length	Eff.Length	E	S	W	T	X	E2	S2
+1	0	321	321	10.116	11	N/A	73	0.022	76		
-1	0	321	321	10.116	11	N/A	73	0.022	76		

Statistics:

Query	Strand	MatID	Expected High Score	Observed High Score	HSPs Reportable	HSPs Reported
+1	0	123 (34.0 bits)	1533 (423.6 bits)	4005	58	
-1	0	123 (34.0 bits)	741 (204.8 bits)	18	0	

Query	Strand	MatID	Neighborhd Words	Word Hits	Excluded Hits	Failed Extensions	Successful Extensions	Overlaps Excluded
+1	0	314	56657	18407	32829	5475	85	
-1	0	314	37893	3357	33503	1084	5	

Database: Non-redundant PDB+GBupdate+GenBank+EMBLupdate+EMBL

Release date: 6:31 AM EST Jan 19, 1996

Posted date: 6:39 AM EST Jan 19, 1996

of letters in database: 449,479,361

of sequences in database: 662,343

of database sequences satisfying E: 3246
No. of states in DFA: 220 (220 KB)
Total size of DFA: 228 KB (256 KB)
Time to generate neighborhood: 0.02u 0.01s 0.03t Real: 00:00:00
No. of processors used: 3
Time to search database: 27.36u 3.37s 30.73t Real: 00:00:40
Total cpu time: 27.49u 3.46s 30.95t Real: 00:00:41

WARNINGS ISSUED: 2

WEST**End of Result Set**

Generate Collection

Print

L1: Entry 1 of 1

File: USPT

Aug 14, 2001

US-PAT-NO: 6274143

DOCUMENT-IDENTIFIER: US 6274143 B1

TITLE: Methods of delaying development of HMFG-associated tumors using anti-idiotypic antibody 11D10

DATE-ISSUED: August 14, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Chatterjee; Malaya	Lexington	KY	40502	
Foon; Kenneth A.	Lexington	KY	40536	

US-CL-CURRENT: 424/155.1; 424/131.1, 424/138.1, 424/139.1, 424/143.1, 424/156.1, 424/174.1, 530/387.2

CLAIMS:

What is claimed is:

1. A method of delaying development of a human milk fat globule (HMFG)-associated tumor in an individual having a low tumor burden of an HMFG-associated tumor, comprising administering to the individual an amount of anti-idiotypic antibody 11D10 sufficient to delay development of said HMFG-associated tumor, wherein 11D10 is produced by a hybridoma cell line deposited at the American Type Culture Collection (ATCC) as Accession No. HB 12020, or progeny thereof, whereby development of said HMFG-associated tumor is delayed.
2. The method of claim 1, wherein the individual is high risk of development of an HMFG-associated tumor.
3. The method of claim 2, wherein the individual is in an adjuvant setting.
4. The method of claim 1, wherein 11D10 is administered with an adjuvant.
5. The method of claim 4, wherein the adjuvant is aluminum hydroxide.
6. The method of claim 1, wherein the HMFG-associated tumor is a breast tumor.
7. The method of claim 1, wherein 11D10 is administered in an amount of about 1 mg to about 4 mg.
8. The method of claim 1, wherein 11D10 is administered in an amount of about 2 mg.
9. The method of claim 1, wherein 11D10 is administered at weekly intervals.
10. The method of claim 1, wherein 11D10 is administered every two weeks.
11. The method of claim 1, wherein 11D10 is heat-treated prior to administration.
12. A method of treatment of a human milk fat globule (HMFG)-associated tumor in

an individual with a low tumor burden of an HMFG-associated tumor, comprising administering to the individual an amount of anti-idiotypic antibody 11D10 sufficient to treat said HMFG-associated tumor, wherein 11D10 is produced by a hybridoma cell line deposited at the American Type Culture Collection (ATCC) as Accession No. HB 12020, or progeny thereof, whereby said HMFG-associated tumor is treated.

13. The method of claim 12, wherein the individual is high risk of development of an HMFG-associated tumor.

14. The method of claim 13, wherein the individual is in an adjuvant setting.

15. The method of claim 12, wherein 11D10 is administered with an adjuvant.

16. The method of claim 15, wherein the adjuvant is aluminum hydroxide.

17. The method of claim 12, wherein the HMFG-associated tumor is a breast tumor.

18. The method of claim 12, wherein 11D10 is administered in an amount of about 1 mg to about 4 mg.

19. The method of claim 12, wherein 11D10 is administered in an amount of about 2 mg.

20. The method of claim 12, wherein 11D10 is administered at weekly intervals.

21. The method of claim 12, wherein 11D10 is administered every two weeks.

22. The method of claim 12, wherein 11D10 is heat-treated prior to administration.

23. The method of claim 1, wherein the antibody has light and heavy chain variable region amino acid sequences in SEQ ID NO:2 and SEQ ID NO:4, respectively.

24. The method of claim 12, wherein the antibody has light and heavy chain variable region amino acid sequences in SEQ ID NO:2 and SEQ ID NO:4, respectively.